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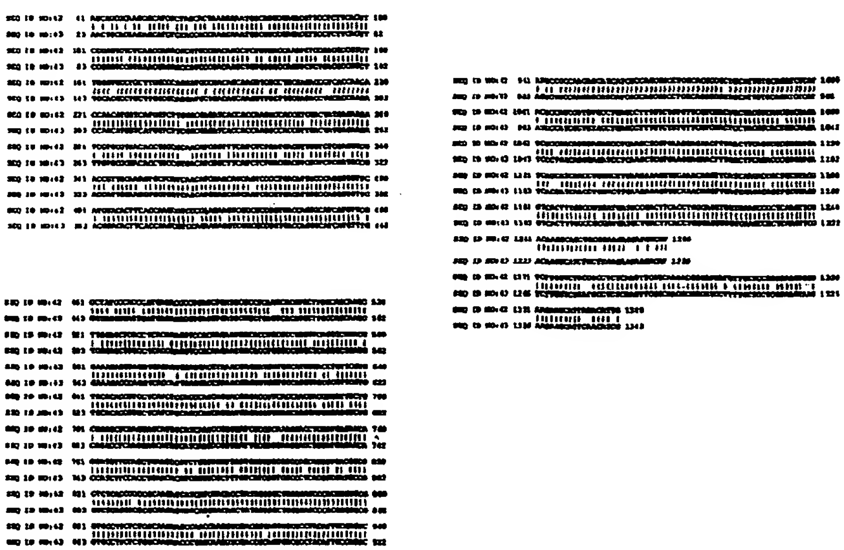

(57) Abstract

This invention relates to an isolated nucleic acid fragment encoding a plant enzyme that catalyzes steps in the biosynthesis of lysine, threonine, methionine, cysteine and isoleucine from aspartate, the enzyme a member selected from the group consisting of: dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase and S-adenosylmethionine synthetase. The invention also relates to the construction of a chimeric gene encoding all or a portion of the enzyme, in sense or antisense orientation, wherein expression of the chimeric gene results in production of altered levels of the enzyme in a transformed host cell.

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TITLE

PLANT AMINO ACID BIOSYNTHETIC ENZYMES

This application claims the benefit of U.S. Provisional Application No. 60/048,771, filed June 6, 1997, and U.S. Provisional Application No. 60/049,443, filed June 12, 1997.

FIELD OF THE INVENTION

This invention is in the field of plant molecular biology. More specifically, this invention pertains to nucleic acid fragments encoding enzymes involved in amino acid biosynthesis in plants and seeds.

BACKGROUND OF THE INVENTION

Many vertebrates, including man, lack the ability to manufacture a number of amino acids and therefore require these amino acids preformed in the diet. These are called essential amino acids. Human food and animal feed, derived from many grains, are deficient in essential amino acids, such as lysine, the sulfur amino acids methionine and cysteine, threonine and tryptophan. For example, in corn (*Zea mays L.*) lysine is the most limiting amino acid for the dietary requirements of many animals. Soybean (*Glycine max L.*) meal is used as an additive to corn-based animal feeds primarily as a lysine supplement. Thus, an increase in the lysine content of either corn or soybean would reduce or eliminate the need to supplement mixed grain feeds with lysine produced via fermentation of microbes. Furthermore, in corn the sulfur amino acids are the third most limiting amino acids, after lysine and tryptophan, for the dietary requirements of many animals. The use of soybean meal, which is rich in lysine and tryptophan, to supplement corn in animal feed is limited by the low sulfur amino acid content of the legume. Thus, an increase in the sulfur amino acid content of either corn or soybean would improve the nutritional quality of the mixtures and reduce the need for further supplementation through addition of more expensive methionine.

Lysine, threonine, methionine, cysteine and isoleucine are amino acids derived from aspartate. Regulation of the biosynthesis of each member of this family is interconnected (see Figure 1). One approach to increasing the nutritional quality of human foods and animal feed is to increase the production and accumulation of specific free amino acids via genetic engineering of this biosynthetic pathway. Alteration of the activity of enzymes in this pathway could lead to altered levels of lysine, threonine, methionine, cysteine and isoleucine. However, few of the genes encoding enzymes that regulate this pathway in plants, especially corn, soybeans and wheat, are available.

The organization of the pathway leading to biosynthesis of lysine, threonine, methionine, cysteine and isoleucine indicates that over-expression or reduction of expression of genes encoding, *inter alia*, threonine synthase, dihydrodipicolinate reductase, diaminopimelate epimerase, threonine deaminase and S-adenosylmethionine synthetase in corn, soybean, wheat and other crop plants could be used to alter levels of these amino acids in human food and animal feed. Accordingly, availability of nucleic acid sequences

encoding all or a portion of these enzymes would facilitate development of nutritionally improved crop plants.

SUMMARY OF THE INVENTION

The instant invention relates to isolated nucleic acid fragments encoding plant enzymes involved in amino acid biosynthesis. Specifically, this invention concerns isolated nucleic acid fragments encoding the following plant enzymes that catalyze steps in the biosynthesis of lysine, threonine, methionine, cysteine and isoleucine from aspartate: dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase and S-adenosylmethionine synthetase. In addition, this invention relates to nucleic acid fragments that are complementary to nucleic acid fragments encoding the listed plant biosynthetic enzymes.

In another embodiment, the instant invention relates to chimeric genes encoding the amino acid biosynthetic acid enzymes listed above or to chimeric genes that comprise nucleic acid fragments that are complementary to the nucleic acid fragments encoding the enzymes, operably linked to suitable regulatory sequences, wherein expression of the chimeric genes results in production of levels of the encoded enzymes in transformed host cells that are altered (i.e., increased or decreased) from the levels produced in untransformed host cells.

In a further embodiment, the instant invention concerns a transformed host cell comprising in its genome a chimeric gene encoding a plant amino acid biosynthetic enzyme operably linked to suitable regulatory sequences, the enzyme selected from the group consisting of: dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase and S-adenosylmethionine synthetase. Expression of the chimeric gene results in production of altered levels of the biosynthetic enzyme in the transformed host cell. The transformed host cells can be of eukaryotic or prokaryotic origin, and include cells derived from higher plants and microorganisms. The invention also includes transformed plants that arise from transformed host cells of higher plants, and seeds derived from such transformed plants.

An additional embodiment of the instant invention concerns a method of altering the level of expression of a plant biosynthetic enzyme in a transformed host cell comprising: a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding a plant biosynthetic enzyme selected from the group consisting of dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase and S-adenosylmethionine synthetase, operably linked to suitable regulatory sequences; and b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of altered levels of the biosynthetic enzyme in the transformed host cell.

An additional embodiment of the instant invention concerns a method for obtaining a nucleic acid fragment encoding all or substantially all of an amino acid sequence encoding a

plant dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase and S-adenosylmethionine synthetase.

A further embodiment of the instant invention is a method for evaluating at least one compound for its ability to inhibit the activity of a plant biosynthetic enzyme selected from the group consisting of dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase and S-adenosylmethionine synthetase, the method comprising the steps of: (a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding a plant biosynthetic enzyme selected from the group consisting of dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase and S-denosylmethionine synthetase, operably linked to suitable regulatory sequences; (b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of the biosynthetic enzyme in the transformed host cell; (c) optionally purifying the biosynthetic enzyme expressed by the transformed host cell; (d) treating the biosynthetic enzyme with a compound to be tested; and (e) comparing the activity of the biosynthetic enzyme that has been treated with a test compound to the activity of an untreated biosynthetic enzyme, thereby selecting compounds with potential for inhibitory activity.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE DESCRIPTIONS

The invention can be more fully understood from the following detailed description and the accompanying drawings and sequence descriptions which form a part of this application.

Figure 1 depicts the biosynthetic pathway for the aspartate family of amino acids. The following abbreviations are used: AK = aspartokinase; ASADH = aspartic semialdehyde dehydrogenase; DHDPS = dihydrodipicolinate synthase; DHDPR = dihydrodipicolinate reductase; DAPEP = diaminopimelate epimerase; DAPDC = diaminopimelate decarboxylase; HDH = homoserine dehydrogenase; HK = homoserine kinase; TS = threonine synthase; TD = threonine deaminase; CγS = cystathionine γ-synthase; CβL = cystathionine β-lyase; MS = methionine synthase; CS = cysteine synthase; and SAMS = S-adenosylmethionine synthase.

Figure 2 shows a multiple alignment of the amino acid sequence fragments reported herein encoding dihydrodipicolinate reductase (SEQ ID NOs:2 and 4) and the *Synechocystis sp.* dihydrodipicolinate reductase sequence set forth in DDBJ Accession No. D90899 (SEQ ID NO:5).

Figure 3 shows a multiple alignment of the amino acid sequence fragments reported herein encoding diaminopimelate epimerase (SEQ ID NOs:7, 9, 11, and 13) and the *Synechocystis sp.* diaminopimelate epimerase sequence set forth in DDBJ Accession No. D90917 (SEQ ID NO:14).

Figure 4 shows a multiple alignment of the amino acid sequence fragments reported herein encoding threonine synthase (SEQ ID NOs:16, 18, 20, 22, 24, and 26) and the *Arabidopsis thaliana* threonine synthase sequence set forth in GenBank Accession No. L41666 (SEQ ID NO:27).

Figure 5 shows a multiple alignment of the amino acid sequence fragments reported herein encoding threonine deaminase (SEQ ID NOs:29, 31, and 33) to the *Brukholderia capacia* threonine synthase set forth in GenBank Accession No. U40630 (SEQ ID NO:34).

Figure 6 shows the nucleotide sequence alignment of the S-adenosylmethionine synthetase reported herein for corn (SEQ ID NO:35) with the *Oryza sativa* S-adenosylmethionine synthetase nucleotide sequence set forth in EMBL Accession No. Z26867 (SEQ ID NO:37).

Figure 7 shows the nucleotide sequence alignment of the S-adenosylmethionine synthetase reported here for soybean (SEQ ID NO:38) with the *Lycopersicon esculentum* S-adenosyl-methionine synthetase nucleotide sequence set forth in EMBL Accession No. Z24741 (SEQ ID NO:40).

Figure 8 shows the nucleotide sequence alignment of the S-adenosylmethionine synthetase reported here for wheat (SEQ ID NO:41) with the *Hordeum vulgare* S-adenosylmethionine synthetase nucleotide sequence set forth in DDBJ Accession No. D63835 (SEQ ID NO:43).

Amino acid sequence alignments were performed using the Clustal method of alignment (Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153), from the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Nucleotide sequence alignments were a result of the BLASTN search performed with each individual S-adenosylmethionine sequence.

The following sequence descriptions and sequence listings attached hereto comply with the rules governing nucleotide and/or amino acid sequence disclosures in patent applications as set forth in 37 C.F.R. §1.821-1.825.

SEQ ID NO:1 is the nucleotide sequence comprising the entire cDNA insert in clone csi1n.pk0042.a3 encoding a corn dihydrodipicolinate reductase.

SEQ ID NO:2 is the deduced amino acid sequence of a portion of a corn dihydrodipicolinate reductase derived from the nucleotide sequence of SEQ ID NO:1.

SEQ ID NO:3 is the nucleotide sequence comprising a portion of the cDNA insert in clone rls2.pk0017.d3 encoding a rice dihydrodipicolinate reductase.

SEQ ID NO:4 is the deduced amino acid sequence of a portion of a rice dihydrodipicolinate reductase derived from the nucleotide sequence of SEQ ID NO:3.

SEQ ID NO:5 is the amino acid sequence of the entire *Synechocystis sp.* dihydrodipicolinate reductase DDBJ Accession No. D90899.

SEQ ID NO:6 is the nucleotide sequence comprising the entire cDNA insert in clone chp2.pk0008.h4 encoding a corn diaminopimelate epimerase.

SEQ ID NO:7 is the deduced amino acid sequence of a portion of a corn diaminopimelate epimerase derived from the nucleotide sequence of SEQ ID NO:6.

SEQ ID NO:8 is the nucleotide sequence comprising a portion of the cDNA insert in clone rls48.pk0036.h10 encoding a rice diaminopimelate epimerase.

SEQ ID NO:9 is the deduced amino acid sequence of a portion of a rice diaminopimelate epimerase derived from the nucleotide sequence of SEQ ID NO:8.

SEQ ID NO:10 is the nucleotide sequence comprising a contig formed of portions of sfl1.pk0031.h3, and sgs1c.pk002.k12, and the entire cDNA insert from clones se2.pk0005.f1, and ses8w.pk0010.h11 encoding a soybean diaminopimelate epimerase.

SEQ ID NO:11 is the deduced amino acid sequence of a soybean diaminopimelate epimerase derived from the nucleotide sequence of SEQ ID NO:10.

SEQ ID NO:12 is the nucleotide sequence comprising a portion of the cDNA insert in clone wlm24.pk0030.g4 encoding a wheat diaminopimelate epimerase.

SEQ ID NO:13 is the deduced amino acid sequence of a portion of a wheat diaminopimelate epimerase derived from the nucleotide sequence of SEQ ID NO:12.

SEQ ID NO:14 is the nucleotide sequence comprising the entire *Synechocystis sp.* diaminopimelate epimerase DDBJ Accession No. D90917.

SEQ ID NO:15 is the nucleotide sequence comprising the entire cDNA insert in clone cc2.pk0031.c9 encoding a corn threonine synthase.

SEQ ID NO:16 is the deduced amino acid sequence of a portion of a corn threonine synthase derived from the nucleotide sequence set forth in SEQ ID NO:15.

SEQ ID NO:17 is the nucleotide sequence comprising part of the cDNA insert in clone cs1.pk0058.g5 encoding a corn threonine synthase.

SEQ ID NO:18 is the deduced amino acid sequence of a portion of a corn threonine synthase derived from the nucleotide sequence of SEQ ID NO:17.

SEQ ID NO:19 is the nucleotide sequence comprising part of the cDNA insert in clone rls72.pk0018.e7 encoding a rice threonine synthase.

SEQ ID NO:20 is deduced amino acid sequence of a portion of a rice threonine synthase derived from the nucleotide sequence set forth in SEQ ID NO:19.

SEQ ID NO:21 is the nucleotide sequence comprising part of the cDNA insert in clone se1.06a03 encoding a soybean threonine synthase.

SEQ ID NO:22 is the deduced amino acid sequence of a portion of a soybean threonine synthase derived from the nucleotide sequence set forth in SEQ ID NO:21.

SEQ ID NO:23 is the nucleotide sequence comprising the entire cDNA insert in clone sr1.pk0003.f6 encoding a soybean threonine synthase.

SEQ ID NO:24 is the deduced amino acid sequence of a portion of a soybean threonine synthase derived from the nucleotide sequence set forth in SEQ ID NO:23.

SEQ ID NO:25 is the nucleotide sequence comprising part of the cDNA insert in clone wr1.pk0085.h2 encoding a wheat threonine synthase.

SEQ ID NO:26 is the deduced amino acid sequence of a portion of a wheat threonine synthase derived from the nucleotide sequence set forth in SEQ ID NO:25.

SEQ ID NO:27 is the entire amino acid sequence of an *Arabidopsis thaliana* threonine synthase found in GenBank Accession No. L41666.

SEQ ID NO:28 is the nucleotide sequence comprising the entire cDNA insert in clone cen1.pk0064.f4 encoding a corn threonine deaminase.

SEQ ID NO:29 is the deduced amino acid sequence of a portion of a corn threonine deaminase derived from the nucleotide sequence set forth in SEQ ID NO:28.

SEQ ID NO:30 is the nucleotide sequence comprising a portion of the cDNA insert in clone sfl1.pk0055.h7 encoding a soybean threonine deaminase.

SEQ ID NO:31 is the deduced amino acid sequence of a portion of a soybean threonine deaminase derived from the nucleotide sequence set forth in SEQ ID NO:30.

SEQ ID NO:32 is the nucleotide sequence comprising the entire cDNA insert in clone sre.pk0044.f3 encoding a soybean threonine deaminase.

SEQ ID NO:33 is the deduced amino acid sequence of a portion of a soybean threonine deaminase derived from the nucleotide sequence set forth in SEQ ID NO:32.

SEQ ID NO:34 is the entire amino acid sequence of a *Burkholderia capacia* threonine deaminase found in GenBank Accession No. U49630.

SEQ ID NO:35 is the nucleotide sequence comprising the entire cDNA insert in clone cc3.mn0002.d2 encoding the entire corn S-adenosylmethionine synthetase.

SEQ ID NO:36 is the deduced amino acid sequence of a corn S-adenosylmethionine synthetase derived from the nucleotide sequence set forth in SEQ ID NO:35.

SEQ ID NO:37 is the entire nucleotide sequence of a *Oryza sativa* S-adenosyl-methionine synthetase found in EMBL Accession No. Z26867.

SEQ ID NO:38 is the nucleotide sequence of the entire cDNA insert in clone s2.12b06 encoding the entire soybean S-adenosyl-methionine synthetase.

SEQ ID NO:39 is the deduced amino acid sequence of the entire soybean S-adenosyl-methionine synthetase derived from the nucleotide sequence set forth in SEQ ID NO:38.

SEQ ID NO:40 is the entire nucleotide sequence of a *Lycopersicon esculentum* S-adenosyl-methionine synthetase found in EMBL Accession No. Z24741.

SEQ ID NO:41 is the nucleotide sequence comprising a contig formed of portions of the cDNA inserts in clones wre1.pk0002.c12, wle1n.pk0070.b8, wkm1c.pk0003.g4, wlk1.pk0028.d3, wre1n.pk170.d8, wr1.pk0086.d5, wr1.pk0103.h8, and wre1n.pk0082.b2 encoding a portion of a wheat S-adenosyl-methionine synthetase.

SEQ ID NO:42 is the deduced amino acid sequence of a wheat S-adenosyl-methionine synthetase derived from the nucleotide sequence set forth in SEQ ID NO:41.

SEQ ID NO:43 is the entire nucleotide sequence of a *Hordeum vulgare* S-adenosyl-methionine synthetase found in DDBJ Accession No. D63835.

The Sequence Descriptions contain the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IYUB standards described in *Nucleic Acids Research 13*:3021-3030 (1985) and in the *Biochemical Journal 219 (No. 2)*:345-373 (1984) which are herein incorporated by reference. The symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. §1.822.

DETAILED DESCRIPTION OF THE INVENTION

In the context of this disclosure, a number of terms shall be utilized. As used herein, an "isolated nucleic acid fragment" is a polymer of RNA or DNA that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. An isolated nucleic acid fragment in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA. As used herein, "contig" refers to an assemblage of overlapping nucleic acid sequences to form one contiguous nucleotide sequence. For example, several DNA sequences can be compared and aligned to identify common or overlapping regions. The individual sequences can then be assembled into a single contiguous nucleotide sequence.

As used herein, "substantially similar" refers to nucleic acid fragments wherein changes in one or more nucleotide bases results in substitution of one or more amino acids, but do not affect the functional properties of the protein encoded by the DNA sequence. "Substantially similar" also refers to nucleic acid fragments wherein changes in one or more nucleotide bases does not affect the ability of the nucleic acid fragment to mediate alteration of gene expression by antisense or co-suppression technology. "Substantially similar" also refers to modifications of the nucleic acid fragments of the instant invention such as deletion or insertion of one or more nucleotides that do not substantially affect the functional properties of the resulting transcript vis-à-vis the ability to mediate alteration of gene expression by antisense or co-suppression technology or alteration of the functional properties of the resulting protein molecule. It is therefore understood that the invention encompasses more than the specific exemplary sequences.

For example, it is well known in the art that antisense suppression and co-suppression of gene expression may be accomplished using nucleic acid fragments representing less that the entire coding region of a gene, and by nucleic acid fragments that do not share 100% identity with the gene to be suppressed. Moreover, alterations in a gene which result in the production of a chemically equivalent amino acid at a given site, but do not effect the functional properties of the encoded protein, are well known in the art. Thus, a codon for the amino acid alanine, a hydrophobic amino acid, may be substituted by a codon encoding another less hydrophobic residue, such as glycine, or a more hydrophobic residue, such as valine, leucine, or isoleucine. Similarly, changes which result in substitution of one negatively charged residue for another, such as aspartic acid for glutamic acid, or one positively charged residue for another, such as lysine for arginine, can also be expected to

produce a functionally equivalent product. Nucleotide changes which result in alteration of the N-terminal and C-terminal portions of the protein molecule would also not be expected to alter the activity of the protein. Each of the proposed modifications is well within the routine skill in the art, as is determination of retention of biological activity of the encoded products. Moreover, the skilled artisan recognizes that substantially similar sequences encompassed by this invention are also defined by their ability to hybridize, under stringent conditions (0.1X SSC, 0.1% SDS, 65°C), with the sequences exemplified herein. Preferred substantially similar nucleic acid fragments of the instant invention are those nucleic acid fragments whose DNA sequences are 80% identical to the DNA sequence of the nucleic acid fragments reported herein. More preferred nucleic acid fragments are 90% identical to the identical to the DNA sequence of the nucleic acid fragments reported herein. Most preferred are nucleic acid fragments that are 95% identical to the DNA sequence of the nucleic acid fragments reported herein. The Clustal multiple alignment alogarithm (Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153) was used here with a GAP PENALTY of 10 and a GAP LENGTH PENALTY of 10.

A "substantial portion" of an amino acid or nucleotide sequence comprises enough of the amino acid sequence of a polypeptide or the nucleotide sequence of a gene to afford putative identification of that polypeptide or gene, either by manual evaluation of the sequence by one skilled in the art, or by computer-automated sequence comparison and identification using algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) J. Mol. Biol. 215:403-410; see also www.ncbi.nlm.nih.gov/BLAST/). In general, a sequence of ten or more contiguous amino acids or thirty or more nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene specific oligonucleotide probes comprising 20-30 contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12-15 bases may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises enough of the sequence to afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches partial or complete amino acid and nucleotide sequences encoding one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

"Codon degeneracy" refers to divergence in the genetic code permitting variation of the nucleotide sequence without effecting the amino acid sequence of an encoded polypeptide. Accordingly, the instant invention relates to any nucleic acid fragment that encodes all or a substantial portion of the amino acid sequence encoding the amino acid biosynthetic enzymes as set forth in SEQ ID NOs:2, 4, 7, 9, 11, 13, 16, 18, 20, 22, 24, 26, 29, 31, and 33. The skilled artisan is well aware of the "codon-bias" exhibited by a specific host cell in usage of nucleotide codons to specify a given amino acid. Therefore, when synthesizing a gene for improved expression in a host cell, it is desirable to design the gene such that its frequency of codon usage approaches the frequency of preferred codon usage of the host cell.

"Synthetic genes" can be assembled from oligonucleotide building blocks that are chemically synthesized using procedures known to those skilled in the art. These building blocks are ligated and annealed to form gene segments which are then enzymatically assembled to construct the entire gene. "Chemically synthesized", as related to a sequence of DNA, means that the component nucleotides were assembled *in vitro*. Manual chemical synthesis of DNA may be accomplished using well established procedures, or automated chemical synthesis can be performed using one of a number of commercially available machines. Accordingly, the genes can be tailored for optimal gene expression based on optimization of nucleotide sequence to reflect the codon bias of the host cell. The skilled artisan appreciates the likelihood of successful gene expression if codon usage is biased towards those codons favored by the host. Determination of preferred codons can be based on a survey of genes derived from the host cell where sequence information is available.

"Gene" refers to a nucleic acid fragment that expresses a specific protein, including regulatory sequences preceding (5' non-coding sequences) and following (3' non-coding sequences) the coding sequence. "Native gene" refers to a gene as found in nature with its own regulatory sequences. "Chimeric gene" refers any gene that is not a native gene, comprising regulatory and coding sequences that are not found together in nature. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are derived from different sources, or regulatory sequences and coding sequences derived from the same source, but arranged in a manner different than that found in nature. "Endogenous gene" refers to a native gene in its natural location in the genome of an organism. A "foreign" gene refers to a gene not normally found in the host organism, but that is introduced into the host organism by gene transfer. Foreign genes can comprise native genes inserted into a non-native organism, or chimeric genes. A "transgene" is a gene that has been introduced into the genome by a transformation procedure.

"Coding sequence" refers to a DNA sequence that codes for a specific amino acid sequence. "Regulatory sequences" refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the

associated coding sequence. Regulatory sequences may include promoters, translation leader sequences, introns, and polyadenylation recognition sequences.

"Promoter" refers to a DNA sequence capable of controlling the expression of a coding sequence or functional RNA. In general, a coding sequence is located 3' to a promoter sequence. The promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence which can stimulate promoter activity and may be an innate element of the promoter or a heterologous element inserted to enhance the level or tissue-specificity of a promoter. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even comprise synthetic DNA segments. It is understood by those skilled in the art that different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. Promoters which cause a gene to be expressed in most cell types at most times are commonly referred to as "constitutive promoters". New promoters of various types useful in plant cells are constantly being discovered; numerous examples may be found in the compilation by Okamuro and Goldberg, (1989) *Biochemistry of Plants 15*:1-82. It is further recognized that since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of different lengths may have identical promoter activity.

The "translation leader sequence" refers to a DNA sequence located between the promoter sequence of a gene and the coding sequence. The translation leader sequence is present in the fully processed mRNA upstream of the translation start sequence. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency. Examples of translation leader sequences have been described (Turner, R. and Foster, G.D. (1995) *Molecular Biotechnology 3*:225).

The "3' non-coding sequences" refer to DNA sequences located downstream of a coding sequence and include polyadenylation recognition sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al., (1989) *Plant Cell 1*:671-680.

"RNA transcript" refers to the product resulting from RNA polymerase-catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA (mRNA)" refers to the RNA that is without introns and that can be translated into protein by the cell. "cDNA" refers to a double-stranded DNA that is complementary to and derived from mRNA. "Sense" RNA refers to RNA transcript that includes the mRNA and so can be translated into protein by the

cell. "Antisense RNA" refers to a RNA transcript that is complementary to all or part of a target primary transcript or mRNA and that blocks the expression of a target gene (U.S. Pat. No. 5,107,065). The complementarity of an antisense RNA may be with any part of the specific gene transcript, i.e., at the 5' non-coding sequence, 3' non-coding sequence, introns, or the coding sequence. "Functional RNA" refers to antisense RNA, ribozyme RNA, or other RNA that is not translated yet has an effect on cellular processes.

The term "operably linked" refers to the association of nucleic acid sequences on a single nucleic acid fragment so that the function of one is affected by the other. For example, a promoter is operably linked with a coding sequence when it is capable of affecting the expression of that coding sequence (i.e., that the coding sequence is under the transcriptional control of the promoter). Coding sequences can be operably linked to regulatory sequences in sense or antisense orientation.

The term "expression", as used herein, refers to the transcription and stable accumulation of sense (mRNA) or antisense RNA derived from the nucleic acid fragment of the invention. Expression may also refer to translation of mRNA into a polypeptide. "Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of the target protein. "Overexpression" refers to the production of a gene product in transgenic organisms that exceeds levels of production in normal or non-transformed organisms. "Co-suppression" refers to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar foreign or endogenous genes (U.S. Patent No. 5,231,020).

"Altered levels" refers to the production of gene product(s) in transgenic organisms in amounts or proportions that differ from that of normal or non-transformed organisms.

"Mature" protein refers to a post-translationally processed polypeptide; i.e., one from which any pre- or propeptides present in the primary translation product have been removed. "Precursor" protein refers to the primary product of translation of mRNA; i.e., with pre- and propeptides still present. Pre- and propeptides may be but are not limited to intracellular localization signals.

A "chloroplast transit peptide" is an amino acid sequence which is translated in conjunction with a protein and directs the protein to the chloroplast or other plastid types present in the cell in which the protein is made. "Chloroplast transit sequence" refers to a nucleotide sequence that encodes a chloroplast transit peptide. A "signal peptide" is an amino acid sequence which is translated in conjunction with a protein and directs the protein to the secretory system (Chrispeels, J.J., (1991) *Ann. Rev. Plant Phys. Plant Mol. Biol. 42*:21-53). If the protein is to be directed to a vacuole, a vacuolar targeting signal (*supra*) can further be added, or if to the endoplasmic reticulum, an endoplasmic reticulum retention signal (*supra*) may be added. If the protein is to be directed to the nucleus, any signal peptide present should be removed and instead a nuclear localization signal included (Raikhel (1992) *Plant Phys. 100*:1627-1632).

"Transformation" refers to the transfer of a nucleic acid fragment into the genome of a host organism, resulting in genetically stable inheritance. Host organisms containing the transformed nucleic acid fragments are referred to as "transgenic" organisms. Examples of methods of plant transformation include Agrobacterium-mediated transformation (De Blaere et al. (1987) *Meth. Enzymol. 143*:277) and particle-accelerated or "gene gun" transformation technology (Klein et al. (1987) *Nature (London) 327*:70-73; U.S. Pat. No. 4,945,050).

Standard recombinant DNA and molecular cloning techniques used herein are well known in the art and are described more fully in Sambrook, J., Fritsch, E.F. and Maniatis, T. *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, 1989 (hereinafter "Maniatis").

Nucleic acid fragments encoding at least a portion of several plant amino acid biosynthetic enzymes have been isolated and identified by comparison of random plant cDNA sequences to public databases containing nucleotide and protein sequences using the BLAST algorithms well known to those skilled in the art. Table 1 lists the amino acid biosynthetic enzymes that are described herein, and the designation of the cDNA clones that comprise the nucleic acid fragments encoding these enzymes.

TABLE 1
Amino Acid Biosynthetic Enzymes

Enzyme	Clone	Plant
dihydrodipicolinate reductase	cs1.pk0083.b10	corn
	rls2.pk0017.d3	rice
diaminopimelate epimerase	chp2.pk0008.h4	corn
	rls48.pk0036.h10	rice
	se2.pk0005.f1	soybean
	ses8w.pk0010.f11	soybean
	sfl1.pk0031.h3	soybean
	sgs1c.pk002.k12	soybean
	wlm24.pk0030.g4	wheat
threonine synthase	cc2.pk0031.c9	corn
	cs1.pk0058.g5	corn
	rls72.pk0018.e7	rice
	se1.06a03	soybean
	sr1.pk0003.f6	soybean
	wr1.pk0085.h2	wheat
threonine deaminase	cen1.pk0064.f4	corn
	sfl1.pk0055.h7	soybean
	sre.pk0044.f3	soybean

Enzyme	Clone	Plant
s-adenosylmethionine synthase	cc3.mn0002.d2	corn
	se2.12b06	soybean
	wre1.pk0002.c12	wheat
	wle1n.pk0070.b8	wheat
	wkm1c.pk0003.g4	wheat
	wlk1.pk0028.d3	wheat
	wre1n.pk170.d8	wheat
	wr1.pk0086.d5	wheat
	wr1.pk0103.h8	wheat
	wre1n.pk0082.b2	wheat

The nucleic acid fragments of the instant invention may be used to isolate cDNAs and genes encoding homologous enzymes from the same or other plant species. Isolation of homologous genes using sequence-dependent protocols is well known in the art. Examples of sequence-dependent protocols include, but are not limited to, methods of nucleic acid hybridization, and methods of DNA and RNA amplification as exemplified by various uses of nucleic acid amplification technologies (e.g., polymerase chain reaction, ligase chain reaction).

For example, genes encoding other amino acid biosynthetic enzymes, either as cDNAs or genomic DNAs, could be isolated directly by using all or a portion of the instant nucleic acid fragments as DNA hybridization probes to screen libraries from any desired plant employing methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the instant nucleic acid sequences can be designed and synthesized by methods known in the art (Maniatis). Moreover, the entire sequences can be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primers DNA labeling, nick translation, or end-labeling techniques. or RNA probes using available *in vitro* transcription systems. In addition, specific primers can be designed and used to amplify a part of or full-length of the instant sequences. The resulting amplification products can be labeled directly during amplification reactions or labeled after amplification reactions, and used as probes to isolate full length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, two short segments of the instant nucleic acid fragments may be used in polymerase chain reaction protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA. The polymerase chain reaction may also be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the instant nucleic acid fragments, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, the skilled artisan can follow

the RACE protocol (Frohman et al., (1988) *PNAS USA 85*:8998) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Primers oriented in the 3' and 5' directions can be designed from the instant sequences. Using commercially available 3' RACE or 5' RACE systems (BRL), specific 3' or 5' cDNA fragments can be isolated (Ohara et al., (1989) *PNAS USA 86*:5673; Loh et al., (1989) *Science 243*:217). Products generated by the 3' and 5' RACE procedures can be combined to generate full-length cDNAs (Frohman, M.A. and Martin, G.R., (1989) *Techniques 1*:165).

Availability of the instant nucleotide and deduced amino acid sequences facilitates immunological screening cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides can be used to immunize animals to produce polyclonal or monoclonal antibodies with specificity for peptides or proteins comprising the amino acid sequences. These antibodies can be then be used to screen cDNA expression libraries to isolate full-length cDNA clones of interest (Lerner, R.A. (1984) *Adv. Immunol. 36*:1; Maniatis).

The nucleic acid fragments of the instant invention may be used to create transgenic plants in which the disclosed biosynthetic enzymes are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of free amino acids in those cells.

Overexpression of the biosynthetic enzymes of the instant invention may be accomplished by first constructing chimeric genes in which the coding region are operably linked to promoters capable of directing expression of a gene in the desired tissues at the desired stage of development. For reasons of convenience, the chimeric genes may comprise promoter sequences and translation leader sequences derived from the same genes. 3' Non-coding sequences encoding transcription termination signals may also be provided. The instant chimeric genes may also comprise one or more introns in order to facilitate gene expression.

Plasmid vectors comprising the instant chimeric genes can then constructed. The choice of plasmid vector is dependent upon the method that will be used to transform host plants. The skilled artisan is well aware of the genetic elements that must be present on the plasmid vector in order to successfully transform, select and propagate host cells containing the chimeric gene. The skilled artisan will also recognize that different independent transformation events will result in different levels and patterns of expression (Jones et al., (1985) *EMBO J. 4*:2411-2418; De Almeida et al., (1989) *Mol. Gen. Genetics 218*:78-86), and thus that multiple events must be screened in order to obtain lines displaying the desired expression level and pattern. Such screening may be accomplished by Southern analysis of DNA, Northern analysis of mRNA expression, Western analysis of protein expression, or phenotypic analysis.

For some applications it may be useful to direct the instant biosynthetic enzymes to different cellular compartments, or to facilitate their secretion from the cell. It is thus envisioned that the chimeric genes described above may be further supplemented by altering the coding sequences to encode enzymes with appropriate intracellular targeting sequences such as transit sequences (Keegstra, K. (1989) *Cell 56*:247-253), signal sequences or sequences encoding endoplasmic reticulum localization (Chrispeels, J.J., (1991) *Ann. Rev. Plant Phys. Plant Mol. Biol. 42*:21-53), or nuclear localization signals (Raikhel, N. (1992) *Plant Phys.100*:1627-1632) added and/or with targeting sequences that are already present removed. While the references cited give examples of each of these, the list is not exhaustive and more targeting signals of utility may be discovered in the future.

It may also be desirable to reduce or eliminate expression of the genes encoding the instant biosynthetic enzymes in plants for some applications. In order to accomplish this, chimeric genes designed for co-suppression of the instant biosynthetic enzymes can be constructed by linking the genes or gene fragments encoding the enzymes to plant promoter sequences. Alternatively, chimeric genes designed to express antisense RNA for all or part of the instant nucleic acid fragments can be constructed by linking the genes or gene fragment in reverse orientation to plant promoter sequences. Either the co-suppression or antisense chimeric genes could be introduced into plants via transformation wherein expression of the corresponding endogenous genes are reduced or eliminated.

The instant amino acid biosynthetic enzymes (or portions of the enzymes) may be produced in heterologous host cells, particularly in the cells of microbial hosts, and can be used to prepare antibodies to the enzymes by methods well known to those skilled in the art. The antibodies are useful for detecting the enzymes *in situ* in cells or *in vitro* in cell extracts. Preferred heterologous host cells for production of the instant amino acid biosynthetic enzymes are microbial hosts. Microbial expression systems and expression vectors containing regulatory sequences that direct high level expression of foreign proteins are well known to those skilled in the art. Any of these could be used to construct chimeric genes for production of the instant amino acid biosynthetic enzymes. These chimeric genes could then be introduced into appropriate microorganisms via transformation to provide high level expression of the enzymes. An example of a vector for high level expression of the instant amino acid biosynthetic enzymes in a bacterial host is provided (Example 11).

Additionally, the instant plant amino acid biosynthetic enzymes can be used as a targets to facilitate design and/or identification of inhibitors of the enzymes that may be useful as herbicides. This is desirable because the enzymes described herein catalyze various steps in a pathway leading to production of several essential amino acids. Accordingly, inhibition of the activity of one or more of the enzymes described herein could lead to inhibition of amino acid biosynthesis sufficient to inhibit plant growth. Thus, the instant plant amino acid biosynthetic enzymes could be appropriate for new herbicide discovery and design.

All or a substantial portion of the nucleic acid fragments of the instant invention may also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. For example, the instant nucleic acid fragments may be used as restriction fragment length polymorphism (RFLP) markers. Southern blots (Maniatis) of restriction-digested plant genomic DNA may be probed with the nucleic acid fragments of the instant invention. The resulting banding patterns may then be subjected to genetic analyses using computer programs such as MapMaker (Lander et at., (1987) *Genomics 1*:174-181) in order to construct a genetic map. In addition, the nucleic acid fragments of the instant invention may be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. Segregation of the DNA polymorphisms is noted and used to calculate the position of the instant nucleic acid sequence in the genetic map previously obtained using this population (Botstein, D. et al., (1980) *Am. J. Hum. Genet. 32*:314-331).

The production and use of plant gene-derived probes for use in genetic mapping is described in R. Bernatzky, R. and Tanksley, S. D. (1986) *Plant Mol. Biol. Reporter 4(1)*:37-41. Numerous publications describe genetic mapping of specific cDNA clones using the methodology outlined above or variations thereof. For example, F2 intercross populations, backcross populations, randomly mated populations, near isogenic lines, and other sets of individuals may be used for mapping. Such methodologies are well known to those skilled in the art.

Nucleic acid probes derived from the instant nucleic acid sequences may also be used for physical mapping (i.e., placement of sequences on physical maps; *see* Hoheisel, J. D., et al., In: *Nonmammalian Genomic Analysis: A Practical Guide*, Academic press 1996, pp. 319-346, and references cited therein).

In another embodiment, nucleic acid probes derived from the instant nucleic acid sequences may be used in direct fluorescence *in situ* hybridization (FISH) mapping (Trask, B. J. (1991) *Trends Genet.* 7:149-154). Although current methods of FISH mapping favor use of large clones (several to several hundred KB; see Laan, M. et al. (1995) *Genome Research 5*:13-20), improvements in sensitivity may allow performance of FISH mapping using shorter probes.

A variety of nucleic acid amplification-based methods of genetic and physical mapping may be carried out using the instant nucleic acid sequences. Examples include allele-specific amplification (Kazazian, H. H. (1989) *J. Lab. Clin. Med. 114(2)*:95-96), polymorphism of PCR-amplified fragments (CAPS; Sheffield, V. C. et al. (1993) *Genomics 16*:325-332), allele-specific ligation (Landegren, U. et al. (1988) *Science 241*:1077-1080), nucleotide extension reactions (Sokolov, B. P. (1990) *Nucleic Acid Res. 18*:3671), Radiation Hybrid Mapping (Walter, M. A. et al. (1997) *Nature Genetics* 7:22-28) and Happy Mapping

(Dear, P. H. and Cook, P. R. (1989) *Nucleic Acid Res. 17*:6795-6807). For these methods, the sequence of a nucleic acid fragment is used to design and produce primer pairs for use in the amplification reaction or in primer extension reactions. The design of such primers is well known to those skilled in the art. In methods employing PCR-based genetic mapping, it may be necessary to identify DNA sequence differences between the parents of the mapping cross in the region corresponding to the instant nucleic acid sequence. This, however, is generally not necessary for mapping methods.

Loss of function mutant phenotypes may be identified for the instant cDNA clones either by targeted gene disruption protocols or by identifying specific mutants for these genes contained in a maize population carrying mutations in all possible genes (Ballinger and Benzer, (1989) *Proc. Natl. Acad. Sci USA 86*:9402; Koes et al., (1995) *Proc. Natl. Acad. Sci USA 92*:8149; Bensen et al., (1995) *Plant Cell 7*:75). The latter approach may be accomplished in two ways. First, short segments of the instant nucleic acid fragments may be used in polymerase chain reaction protocols in conjunction with a mutation tag sequence primer on DNAs prepared from a population of plants in which Mutator transposons or some other mutation-causing DNA element has been introduced (see Bensen, *supra*). The amplification of a specific DNA fragment with these primers indicates the insertion of the mutation tag element in or near the plant gene encoding dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase or S-adenosyl-methionine synthetase. Alternatively, the instant nucleic acid fragment may be used as a hybridization probe against PCR amplification products generated from the mutation population using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer, such as that for a restriction enzyme site-anchored synthetic adaptor. With either method, a plant containing a mutation in the endogenous gene encoding a dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase or S-adenosylmethionine synthetase can be identified and obtained. This mutant plant can then be used to determine or confirm the natural function of the dihydro-dipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase and S-adenosylmethionine synthetase gene product.

EXAMPLES

The present invention is further defined in the following Examples, in which all parts and percentages are by weight and degrees are Celsius, unless otherwise stated. It should be understood that these Examples, while indicating preferred embodiments of the invention, are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions.

EXAMPLE 1

Composition of cDNA Libraries; Isolation and Sequencing of cDNA Clones

cDNA libraries representing mRNAs from various corn, rice, soybean and wheat tissues were prepared. The characteristics of the libraries are described below.

TABLE 2

cDNA Libraries from Corn and Soybean Tissues

Library	Tissue	Clone
cc2	Corn Callus, Partially Differentiated, 2 Weeks After Subculture	cc2.pk0031.c9
cc3	Corn Callus, Mature Somatic Embryo	cc3.mn0002.d2
cen1	Corn Endosperm 12 Days After Pollination	cen1.pk0064.f4
chp2	Corn Leaf, 11 Day Old Plant	chp2.pk0008.h4
cs1	Corn Leaf, Sheath 5 Week Old Plant	cs1.pk0058.g5
csi1n	Corn Silk*	csi1n.pk0042.a3
rls2	Rice Leaf 15 Days After Germination, 2 Hours After Infection of Strain Magaporthe grisea 4360-R-67 (AVR2-YAMO); Susceptible	rls2.pk0017.d3
rls48	Rice Leaf 15 Days After Germination, 48 Hours After Infection of Strain Magaporthe grisea 4360-R-67 (AVR2-YAMO); Susceptible	rls48.pk0036.h10
rls72	Rice Leaf 15 Days After Germination, 72 Hours After Infection of Strain Magaporthe grisea 4360-R-67 (AVR2-YAMO); Susceptible	rls72.pk0018.e7
s2	Soybean Seed, 19 Days After Flowering	s2.12b06
se1	Soybean Embryo 7 Days After Flowering	se1.06a03
se2	Soybean Embryo 10 Days After Flowering	se2.pk0005.f1
ses8w	Mature Soybean Embryo 8 Weeks After Subculture	ses8w.pk0010.h11
sfl1	Soybean Immature Flower	sfl1.pk0055.h7 sfl1.pk0031.h3
sgs1c	Soybean Seeds 4 Hours After Germination	sgs1c.pk002.k12
sr1	Soybean Root From 10 Day Old Seedlings	sr1.pk0003.f6
sre	Soybean Root Elongation 4-5 Days After Germination	sre.pk0044.f3
wkm1c	Wheat Kernel Malted 55 Hours at 22 Degrees Celsius	wkm1c.pk0003.g4
wle1n	Wheat Leaf From 7 Day Old Etiolated Seedling*	wle1n.pk0070.b8
wlk1	Wheat Seedlings 1 Hour After Treatment with Fungicide**	wlk1.pk0028.d3
wlm24	Wheat Seedlings 24 Hours After Inoculation With Erysiphe graminis f. sp tritici	wlm24.pk0030.g4
wr1	Wheat Root From 7 Day Old Seedling	wr1.pk0085.h2 wr1.pk0086.d5 wr1.pk0103.h8
wre1	Wheat Root From 7 Day Old Etiolated Seedling	wre1.pk0002.c12
wre1n	Wheat Root From 7 Day Old Etiolated Seedling*	wre1n.pk0082.b2 wre1n.pk170.d8

*These libraries were normalized essentially as described in U.S. Pat. No. 5,482,845

**Application of 6-iodo-2-propoxy-3-propyl-4(3*H*)-quinazolinone; synthesis and methods of using this compound are described in USSN 08/545,827, incorporated herein by reference.

cDNA libraries were prepared in Uni-ZAP™ XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems,La Jolla, CA). Conversion of the Uni-ZAP™ XR libraries into plasmid libraries was accomplished according to the protocol provided by Stratagene. Upon conversion, cDNA inserts were contained in the plasmid vector pBluescript. cDNA inserts from randomly picked bacterial colonies containing recombinant pBluescript plasmids were amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences, or plasmid DNA was prepared from cultured bacterial cells. Amplified insert DNAs or plasmid DNAs were sequenced in dye-primer sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"; see Adams, M. D. et al., (1991) *Science 252*:1651). The resulting ESTs were analyzed using a Perkin Elmer Model 377 fluorescent sequencer.

EXAMPLE 2

Identification and Characterization of cDNA Clones

ESTs encoding plant amino acid biosynthetic enzymes were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) *J. Mol. Biol. 215*:403-410; see also www.ncbi.nlm.nih.gov/BLAST/) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. (1993) *Nature Genetics 3*:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

EXAMPLE 3

Characterization of cDNA Clones Encoding Polypeptides Homologous to Dihydrodipicolinate Reductase

The BLASTX search using the nucleotide sequences from clones csi1n.pk0042.a3 and rls2.pk0017.d3 revealed similarity of the protein encoded by the cDNA to *Synechocystis sp.*

dihydrodipicolinate reductase enzyme (DDBJ Accession No. D90899). BLAST pLog values were 12.60 and 11.68 for csi1n.pk0042.a3 and rls2.pk0017.d3, respectively.

The sequence of the entire cDNA insert in clone csi1n.pk0042.a3 was determined and is shown in SEQ ID NO:1; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:2. The amino acid sequence set forth in SEQ ID NO:2 was evaluated by BLASTP, yielding a pLog value of 36.72 versus the *Synechocystis sp.* dihydrodipicolinate reductase sequence. The sequence of a portion of the cDNA insert from clone rls2.pk0017.d3 is shown in SEQ ID NO:3; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:4. Figure 2 presents an alignment of the amino acid sequences set forth in SEQ ID NO:2 and the *Synechocystis sp.* dihydrodipicolinate reductase sequence (SEQ ID NO:5). SEQ ID NO:2 is 40% identical to the *Synechocystis sp.* dihydrodipicolinate reductase sequence (SEQ ID NO:5). Sequence alignments were performed by the Clustal method of alignment (Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153), using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Sequence percent identity calculations were performed by the Jotun Hein method (Hein. J. J. (1990) *Meth. Enz. 183*:626-645) using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI).

Sequence alignments and BLAST scores and probabilities indicate that the instant nucleic acid fragments encode a nearly entire corn dihydropicolinate reductase, and a portion of a rice dihydropicolinate reductase. These sequences represent the first plant sequences encoding dihydropicolinate reductase.

EXAMPLE 4

Characterization of cDNA Clones Encoding Diaminopimelate Epimerase

The BLASTX search using the nucleotide sequences from clones chp2.pk0008.h4, rls48.pk0036.h10, wlm24.pk0030.g4, and the contig sequences assembled from clones se2.pk0005.f1, ses8w.pk0010.h11,sfl1.pk0031.h3, and sgs1c.pk002.k12 revealed similarity of the proteins encoded by the cDNAs to diaminopimelate epimerase from *Synechocystis sp.* (DDBJ Accession No. D90917). The BLAST results for each of these ESTs are shown in Table 3:

TABLE 3

BLAST Results for Clones Encoding Polypeptides Homologous to Diaminopimelate Epimerase

Clone	BLAST pLog Score DDBJ Accession No. D90917
chp2.pk0008.h4	59.16
rls48.pk0036.h10	40.82
The contig of: se2.pk0005.f1 ses8w.pk0010.h11 sfl1.pk0031.h3 sgs1c.pk002.k12	98.30
wlm24.pk0030.g4	23.46

The sequence of the entire cDNA insert in clone chp2.pk0008.h4 was determined and is shown in SEQ ID NO:6; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:7. The amino acid sequence set forth in SEQ ID NO:7 was evaluated by BLASTP, yielding a pLog value of 75.66 versus the *Synechocystis sp.* sequence. The sequence of a portion of the cDNA insert from clone rls48.pk0036.h10 is shown in SEQ ID NO:8; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:9. The nucleotide sequence of the contig assembled from clones se2.pk0005.f1, ses8w.pk0010.h11, sfl1.pk0031.h3, and sgs1c.pk002.k12 was determined and is shown in SEQ ID NO:10; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:11. The amino acid sequence set forth in SEQ ID NO:11 was evaluated by BLASTP, yielding a pLog value of 98.57 versus the *Synechocystis sp.* sequence. The sequence of a portion of the cDNA insert from clone wlm24.pk0030.g4 is shown in SEQ ID NO.12; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:13. Figure 3 presents an alignment of the amino acid sequences set forth in SEQ ID NOs:7, 9, 11, and 13 and the *Synechocystis sp.* sequence (SEQ ID NO:14). The data in Table 4 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs: 7, 9, 11, and 13 and the *Synechocystis sp.* sequence.

TABLE 4

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to Diaminopimelate Epimerase

Clone	SEQ ID NO.	Percent Identity to DDBJ Accession No. D90917 (SEQ ID NO:16)
chp2.pk0008.h4	7	59
rls48.pk0036.h10	9	74
Contig of: se2.pk0005.f1 ses8w.pk0010.h11 sfl1.pk0031.h3 sgs1c.pk002.k12	11	72
wlm24.pk0030.g4	13	65

Sequence alignments were performed by the Clustal method of alignment (Higgins, D.G. and Sharp, P.M. (1989) CABIOS 5:151-153), using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Sequence percent identity calculations were performed by the Jotun Hein method (Hein. J. J. (1990) Meth. Enz. 183:626-645) using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI).

Sequence alignments and BLAST scores and probabilities indicate that the instant nucleic acid fragments encode a nearly entire corn diaminopimelate epimerase (chp2.pk0008.h4), a portion of a rice diaminopimelate epimerase (rls48.pk0036.h10), and an entire soybean diaminopimelate epimerase (se2.pk0005.f1, ses8w.pk0010.h11, sfl1.pk0031.h3, and sgs1c.pk002.k12), and a portion of a wheat diaminopimelate epimerase (wlm24.pk0030.g4). These sequences represent the first plant sequences encoding diaminopimelate epimerase enzyme.

EXAMPLE 5

Characterization of cDNA Clones Encoding Threonine Synthase

The BLASTX search using the EST sequences from clones cc2.pk0031.c9, cs1.pk0058.g5, rls72.pk0018.e7, se1.06a03, sr1.pk0003.f6, and wr1.pk0085.h2 revealed similarity of the proteins encoded by the cDNAs to threonine synthase from *Arabidopsis thaliana* (*GenBank* Accession No. L41666). The BLAST results for each of these ESTs are shown in Table 5:

TABLE 5

BLAST Results for Clones Encoding Polypeptides Homologous to Threonine Synthase

Clone	BLAST pLog Score L41666
cc2.pk0031.c9	56.19
cs1.pk0058.g5	8.00
rls72.pk0018.e7	29.47
se1.06a03	34.15
sr1.pk0003.f6	21.13
wr1.pk0085.h2	29.47

The sequence of the entire cDNA insert in clone cc2.pk0031.c9 was determined and is shown in SEQ ID NO:15; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:16. The amino acid sequence set forth in SEQ ID NO:16 was evaluated by BLASTP, yielding a pLog value of 166.11 versus the *Arabidopsis thaliana* sequence. BLASTN against dbest indicated identity of nucleotides 520 through 684 from cc2.pk0031.c9 with nucleotides 1 through 162 of a corn EST (GenBank Accession No. T18847). The sequence of a portion of the cDNA insert from clone cs1.pk0058.g5 is shown in SEQ ID NO:17; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:18. The sequence of a portion of the cDNA insert from clone rls72.pk0018.e7 is shown in SEQ ID NO:19; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:20. The sequence of a portion of the cDNA insert from clone se1.06a03 is shown in SEQ ID NO:21; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:22. The sequence of the entire cDNA insert in clone sr1.pk0003.f6 was determined and is shown in SEQ ID NO:23; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:24. The amino acid sequence set forth in SEQ ID NO:24 was evaluated by BLASTP, yielding a pLog value of 275.06 versus the *Arabidopsis thaliana* sequence. The sequence of a portion of the cDNA insert from clone wr1.pk0085.h2 is shown in SEQ ID NO:25; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:26. Figure 4 presents an alignment of the amino acid sequences set forth in SEQ ID NOs:16, 18, 20, 22, 24, and 26 and the *Arabidopsis thaliana* sequence. The data in Table 6 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:16, 18, 20, 22, 24, and 26 and the *Arabidopsis thaliana* sequence (SEQ ID NO:27).

TABLE 6

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to Threonine Synthase

Clone	SEQ ID NO.	Percent Identity to L41666 (SEQ ID NO:29)
cc2.pk0031.c9	16	81.0
cs1.pk0058.g5	18	81.0
rls72.pk0018.e7	20	55.3
se1.06a03	22	80.0
sr1.pk0003.f6	24	84.4
wr1.pk0085.h2	26	50.4

Sequence alignments were performed by the Clustal method of alignment (Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153), using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Sequence percent identity calculations were performed by the Jotun Hein method (Hein. J. J. (1990) *Meth. Enz. 183*:626-645) using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI).

Sequence alignments and BLAST scores and probabilities indicate that the instant nucleic acid fragments encode portions of a corn threonine synthase (cc2.pk0031.c9 and cs1.pk0058.g5), a portion of a rice threonine synthase (rls72.pk0018.e7), portions of a soybean threonine synthase (se1.06a03 and sr1.pk0003.f6), and a portion of a wheat threonine synthase (wr1.pk0085.h2). These sequences represent the first corn, rice, soybean, and wheat sequences encoding threonine synthase.

EXAMPLE 6

Characterization of cDNA Clones Encoding Threonine Deaminase

The BLASTX search using the EST sequence from clone cen1.pk0064.f4 revealed similarity of the protein encoded by the cDNA to threonine deaminase from *Brukholderia capacia* (GenBank Accession No. U40630; pLog = 31.38). The BLASTX search using the EST sequences from clones sfl1.pk0055.h7 and sre.pk0044.f3 revealed similarity of the proteins encoded by the cDNAs to threonine deaminase from *Solanum tuberosum* and *Brukholderia capacia* (EMBL Accession No. X67846 and GenBank Accession No. U40630, respectively). BLAST pLog values were 36.55 and 31.79 for sfl1.pk0055.h7, and 19.47 and 14.51 for sre.pk0044.f3.

The sequence of the entire cDNA insert in clone cen1.pk0064.f4 was determined and is shown in SEQ ID NO:28; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:29. The amino acid sequence set forth in SEQ ID NO:29 was evaluated by BLASTP, yielding a pLog value of 134.85 versus the *Brukholderia capacia* sequence. The sequence of a portion of the cDNA insert from clone sfl1.pk0055.h7 is shown in SEQ ID

NO:30; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:31. The sequence of the entire cDNA insert in clone sre.pk0044.f3 was determined and is shown in SEQ ID NO:32; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:33. The amino acid sequence set forth in SEQ ID NO:33 was evaluated by BLASTP, yielding pLog values of *19.24* versus the *Solanum tuberosum* sequence and *15.19* versus the *Brukholderia capacia* threonine deaminase sequence. Figure 5 presents an alignment of the amino acid sequences set forth in SEQ ID NOs:29, 31, and 33 and the *Brukholderia capacia* (SEQ IDNO:34) sequence. The data in Table 7 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:29, 31, and 33 35and the *Brukholderia capacia* sequence.

TABLE 7

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to Threonine Deaminase

Clone	SEQ ID NO.	Percent Identity to U40630 (SEQ ID NO:36)
cen1.pk0064.f4	29	61.0
sfl1.pk0055.h7	31	47.9
sre.pk0044.f3	33	46.0

Sequence alignments were performed by the Clustal method of alignment (Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153), using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Sequence percent identity calculations were performed by the Jotun Hein method (Hein. J. J. (1990) *Meth. Enz. 183*:626-645) using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI)

Sequence alignments and BLAST scores and probabilities indicate that the instant nucleic acid fragments encode a nearly entire corn threonine deaminase (cen1.pk0064.f4) and portions of a soybean threonine deaminase (sfl1.pk0055.h7 and sre.pk0044.f3). These sequences represent the first corn and soybean sequences encoding threonine deaminase.

EXAMPLE 7

Characterization of cDNA Clones Encoding S-adenosylmethionine synthetase

The BLASTX search using the nucleotide sequence from clone cc3.mn0002.d2 revealed similarity of the protein encoded by the cDNA to S-adenosylmethionine synthetase from *Oryza sativa* (EMBL Accession No. Z26867; pLog = 99.03). The sequence of the entire cDNA insert in clone cc3.mn0002.d2 was determined and is shown in SEQ ID NO:35; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:36. The nucleotide sequence set forth in SEQ ID NO:35 was evaluated by BLASTN, yielding a pLog value larger than 200 versus the *Oryza sativa* sequence. Figure 6 presents an alignment of the

nucleotide sequences set forth in SEQ ID NO:35 and the *Oryza sativa* sequence (SEQ ID NO:37). The nucleotide sequence in SEQ ID NO:35 is 88% identical over 1216 nucleotides to the nucleotide sequence of the *Oryza sativa* S-adenosylmethionine synthetase.

The BLASTX search using the nucleotide sequence from clone s2.12b06 revealed similarity of the protein encoded by the cDNA to S-adenosylmethionine synthetase from *Lycopersicon esculentum* (EMBL Accession No. Z24741; pLog = 62.62). The sequence of the entire cDNA insert in clone s2.12b06 was determined and is shown in SEQ ID NO:38; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:39. The nucleotide sequence set forth in SEQ ID NO:38 was evaluated by BLASTN, yielding a pLog value larger than 200 versus the *Lycopersicon esculentum* sequence. Figure 7 presents an alignment of the nucleotide sequences set forth in SEQ ID NO:38 and the *Lycopersicon esculentum* sequence (SEQ ID NO:40). The nucleotide sequence set forth in SEQ ID NO:38 is 82 % identical over 1210 nucleotides to the *Lycopersicon esculentum* sequence.

The BLASTX search using the nucleotide sequence from the contig assembled from clones wre1.pk0002.c12, wle1n.pk0070.b8, wkm1c.pk0003.g4, wlk1.pk0028.d3, wre1n.pk170.d8, wr1.pk0086.d5, wr1.pk0103.h8, and wre1n.pk0082.b2 revealed similarity of the protein encoded by the contig to S-adenosylmethionine synthetase from *Hordeum vulgare* (DDBJ Accession No. D63835) with a pLog value larger than 200. The nucleotide sequence of the contig assembled from clones wre1.pk0002.c12, wle1n.pk0070.b8, wkm1c.pk0003.g4, wlk1.pk0028.d3, wre1n.pk170.d8, wr1.pk0086.d5, wr1.pk0103.h8, and wre1n.pk0082.b2 is shown in SEQ ID NO:41; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:42. Figure 8 presents an alignment of the nucleotide sequence set forth in SEQ ID NO:41 and the *Hordeum vulgare* sequence (SEQ ID NO:43). The SEQ ID NO:41 is 92% identical to the *Hordeum vulgare* sequence.

Sequence alignments and BLAST scores and probabilities indicate that the instant nucleic acid fragments encode entire or nearly entire corn, soybean, or wheat S-adenosyl-methionine synthetase. These sequences represent the first corn, soybean, or wheat sequences encoding S-adenosylmethionine synthetase.

EXAMPLE 8

Expression of Chimeric Genes in Monocot Cells

A chimeric gene comprising a cDNA encoding an amino acid biosynthetic enzyme in sense orientation with respect to the maize 27 kD zein promoter that is located 5' to the cDNA fragment, and the 10 kD zein 3' end that is located 3' to the cDNA fragment, can be constructed. The cDNA fragment of this gene may be generated by polymerase chain reaction (PCR) of the cDNA clone using appropriate oligonucleotide primers and under appropriate experimental conditions. Cloning sites (NcoI or SmaI) can be incorporated into the oligonucleotides to provide proper orientation of the DNA fragment when inserted into the digested vector pML103 as described below. The amplified DNA can then be digested with restriction enzymes NcoI and SmaI and fractionated on a 0.7% low melting point

agarose gel in 40 mM Tris-acetate, pH 8.5, 1 mM EDTA. The appropriate band can be excised from the gel, melted at 68°C and combined with a 4.9 kb NcoI-SmaI fragment of the plasmid pML103. Plasmid pML103 has been deposited under the terms of the Budapest Treaty at ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209), and bears accession number ATCC 97366. The DNA segment from pML103 contains a 1.05 kb SalI-NcoI promoter fragment of the maize 27 kD zein gene and a 0.96 kb SmaI-SalI fragment from the 3' end of the maize 10 kD zein gene in the vector pGem9Zf(+) (Promega). Vector and insert DNA can be ligated at 15°C overnight, essentially as described (Maniatis). The ligated DNA may then be used to transform *E. coli* XL1-Blue (Epicurian Coli XL-1 Blue™; Stratagene). Bacterial transformants can be screened by restriction enzyme digestion of plasmid DNA and limited nucleotide sequence analysis using the dideoxy chain termination method (Sequenase™ DNA Sequencing Kit; U.S. Biochemical). The resulting plasmid construct would comprise a chimeric gene encoding, in the 5' to 3' direction, the maize 27 kD zein promoter, a cDNA fragment encoding a plant amino acid biosynthetic enzyme, and the 10 kD zein 3' region.

The chimeric gene described above can then be introduced into corn cells by the following procedure. Immature corn embryos can be dissected from developing caryopses derived from crosses of the inbred corn lines H99 and LH132. The embryos are isolated 10 to 11 days after pollination when they are 1.0 to 1.5 mm long. The embryos are then placed with the axis-side facing down and in contact with agarose-solidified N6 medium (Chu et al., (1975) *Sci. Sin. Peking* 18:659-668). The embryos are kept in the dark at 27°C. Friable embryogenic callus consisting of undifferentiated masses of cells with somatic proembryoids and embryoids borne on suspensor structures proliferates from the scutellum of these immature embryos. The embryogenic callus isolated from the primary explant can be cultured on N6 medium and sub-cultured on this medium every 2 to 3 weeks.

The plasmid, p35S/Ac (obtained from Dr. Peter Eckes, Hoechst Ag, Frankfurt, Germany) may be used in transformation experiments in order to provide for a selectable marker. This plasmid contains the *Pat* gene (see European Patent Publication 0 242 236) which encodes phosphinothricin acetyl transferase (PAT). The enzyme PAT confers resistance to herbicidal glutamine synthetase inhibitors such as phosphinothricin. The *pat* gene in p35S/Ac is under the control of the 35S promoter from Cauliflower Mosaic Virus (Odell et al. (1985) *Nature* 313:810-812) and the 3' region of the nopaline synthase gene from the T-DNA of the Ti plasmid of *Agrobacterium tumefaciens*.

The particle bombardment method (Klein et al., (1987) *Nature* 327:70-73) may be used to transfer genes to the callus culture cells. According to this method, gold particles (1 µm in diameter) are coated with DNA using the following technique. Ten µg of plasmid DNAs are added to 50 µL of a suspension of gold particles (60 mg per mL). Calcium chloride (50 µL of a 2.5 M solution) and spermidine free base (20 µL of a 1.0 M solution) are added to the particles. The suspension is vortexed during the addition of these solutions.

After 10 minutes, the tubes are briefly centrifuged (5 sec at 15,000 rpm) and the supernatant removed. The particles are resuspended in 200 μL of absolute ethanol, centrifuged again and the supernatant removed. The ethanol rinse is performed again and the particles resuspended in a final volume of 30 μL of ethanol. An aliquot (5 μL) of the DNA-coated gold particles can be placed in the center of a Kapton™ flying disc (Bio-Rad Labs). The particles are then accelerated into the corn tissue with a Biolistic™ PDS-1000/He (Bio-Rad Instruments, Hercules CA), using a helium pressure of 1000 psi, a gap distance of 0.5 cm and a flying distance of 1.0 cm.

For bombardment, the embryogenic tissue is placed on filter paper over agarose-solidified N6 medium. The tissue is arranged as a thin lawn and covered a circular area of about 5 cm in diameter. The petri dish containing the tissue can be placed in the chamber of the PDS-1000/He approximately 8 cm from the stopping screen. The air in the chamber is then evacuated to a vacuum of 28 inches of Hg. The macrocarrier is accelerated with a helium shock wave using a rupture membrane that bursts when the He pressure in the shock tube reaches 1000 psi.

Seven days after bombardment the tissue can be transferred to N6 medium that contains gluphosinate (2 mg per liter) and lacks casein or proline. The tissue continues to grow slowly on this medium. After an additional 2 weeks the tissue can be transferred to fresh N6 medium containing gluphosinate. After 6 weeks, areas of about 1 cm in diameter of actively growing callus can be identified on some of the plates containing the glufosinate-supplemented medium. These calli may continue to grow when sub-cultured on the selective medium.

Plants can be regenerated from the transgenic callus by first transferring clusters of tissue to N6 medium supplemented with 0.2 mg per liter of 2,4-D. After two weeks the tissue can be transferred to regeneration medium (Fromm et al., (1990) *Bio/Technology* *8*:833-839).

EXAMPLE 9

Expression of Chimeric Genes in Dicot Cells

A seed-specific expression cassette composed of the promoter and transcription terminator from the gene encoding the β subunit of the seed storage protein phaseolin from the bean *Phaseolus vulgaris* (Doyle et al. (1986) *J. Biol. Chem. 261*:9228-9238) can be used for expression of the instant amino acid biosynthetic enzymes in transformed soybean. The phaseolin cassette includes about 500 nucleotides upstream (5') from the translation initiation codon and about 1650 nucleotides downstream (3') from the translation stop codon of phaseolin. Between the 5' and 3' regions are the unique restriction endonuclease sites Nco I (which includes the ATG translation initiation codon), Sma I, Kpn I and Xba I. The entire cassette is flanked by Hind III sites.

The cDNA fragment of this gene may be generated by polymerase chain reaction (PCR) of the cDNA clone using appropriate oligonucleotide primers. Cloning sites can be

incorporated into the oligonucleotides to provide proper orientation of the DNA fragment when inserted into the expression vector. Amplification is then performed, and the isolated fragment is inserted into a pUC18 vector carrying the seed expression cassette.

Plant amino acid biosynthetic enzymes are known to be localized in the chloroplasts. Accordingly, for those enzymes (or polypeptides representing part of the instant amino acid biosynthetic enzymes) that lack a chloroplast targeting signal, the DNA fragment to be inserted into the expression vector can be synthesized by PCR with primers encoding a chloroplast targeting signal. For example, a chloroplast transit sequence equivalent to the cts of the small subunit of ribulose 1,5-bisphosphate carboxylase from soybean (Berry-Lowe et al. (1982) *J. Mol. Appl. Genet. 1*:483-498) may be used.

Soybean embroys may then be transformed with the expression vector comprising sequences encoding a plant amino acid biosynthetic enzyme. To induce somatic embryos, cotyledons, 3-5 mm in length dissected from surface sterilized, immature seeds of the soybean cultivar A2872, can be cultured in the light or dark at 26°C on an appropriate agar medium for 6-10 weeks. Somatic embryos which produce secondary embryos are then excised and placed into a suitable liquid medium. After repeated selection for clusters of somatic embryos which multiplied as early, globular staged embryos, the suspensions are maintained as described below.

Soybean embryogenic suspension cultures can maintained in 35 mL liquid media on a rotary shaker, 150 rpm, at 26°C with florescent lights on a 16:8 hour day/night schedule. Cultures are subcultured every two weeks by inoculating approximately 35 mg of tissue into 35 mL of liquid medium.

Soybean embryogenic suspension cultures may then be transformed by the method of particle gun bombardment (Kline et al. (1987) *Nature* (London) *327*.70, U.S. Patent No. 4,945,050). A Du Pont Biolistic™ PDS1000/HE instrument (helium retrofit) can be used for these transformations.

A selectable marker gene which can be used to facilitate soybean transformation is a chimeric gene composed of the 35S promoter from Cauliflower Mosaic Virus (Odell et al.(1985) *Nature 313*:810-812), the hygromycin phosphotransferase gene from plasmid pJR225 (from *E. coli*; Gritz et al.(1983) *Gene 25*:179-188) and the 3' region of the nopaline synthase gene from the T-DNA of the Ti plasmid of *Agrobacterium tumefaciens*. The seed expression cassette comprising the phaseolin 5' region, the fragment encoding the biosynthetic enzyme and the phaseolin 3' region can be isolated as a restriction fragment. This fragment can then be inserted into a unique restriction site of the vector carrying the marker gene.

To 50 μL of a 60 mg/mL 1 μm gold particle suspension is added (in order): 5 μL DNA (1 μg/μL), 20 μl spermidine (0.1 M), and 50 μL $CaCl_2$ (2.5 M). The particle preparation is then agitated for three minutes, spun in a microfuge for 10 seconds and the supernatant removed. The DNA-coated particles are then washed once in 400 μL 70% ethanol and

resuspended in 40 μL of anhydrous ethanol. The DNA/particle suspension can be sonicated three times for one second each. Five μL of the DNA-coated gold particles are then loaded on each macro carrier disk.

Approximately 300-400 mg of a two-week-old suspension culture is placed in an empty 60x15 mm petri dish and the residual liquid removed from the tissue with a pipette. For each transformation experiment, approximately 5-10 plates of tissue are normally bombarded. Membrane rupture pressure is set at 1100 psi and the chamber is evacuated to a vacuum of 28 inches mercury. The tissue is placed approximately 3.5 inches away from the retaining screen and bombarded three times. Following bombardment, the tissue can be divided in half and placed back into liquid and cultured as described above.

Five to seven days post bombardment, the liquid media may be exchanged with fresh media, and eleven to twelve days post bombardment with fresh media containing 50 mg/mL hygromycin. This selective media can be refreshed weekly. Seven to eight weeks post bombardment, green, transformed tissue may be observed growing from untransformed, necrotic embryogenic clusters. Isolated green tissue is removed and inoculated into individual flasks to generate new, clonally propagated, transformed embryogenic suspension cultures. Each new line may be treated as an independent transformation event. These suspensions can then be subcultured and maintained as clusters of immature embryos or regenerated into whole plants by maturation and germination of individual somatic embryos.

EXAMPLE 10

Analysis of Amino Acid Content of the Seeds of Transformed Plants

To analyze for expression of the chimeric genes in seeds and for the consequences of expression on the amino acid content in the seeds, a seed meal can be prepared by any of a number of suitable methods known to those skilled in the art. The seed meal can be partially or completely defatted, via hexane extraction for example, if desired. Protein extracts can be prepared from the meal and analyzed for enzyme activity. Alternatively the presence of any of the expressed enzymes can be tested for immunologically by methods well-known to those skilled in the art. To measure free amino acid composition of the seeds, free amino acids can be extracted from the meal and analyzed by methods known to those skilled in the art (Bieleski et al. (1966) Anal. *Biochem.* *17*:278-293). Amino acid composition can then be determined using any commercially available amino acid analyzer. To measure total amino acid composition of the seeds, meal containing both protein-bound and free amino acids can be acid hydrolyzed to release the protein-bound amino acids and the composition can then be determined using any commercially available amino acid analyzer. Seeds expressing the instant amino acid biosynthetic enzymes and with altered lysine, threonine, methionine, cysteine and/or isoleucine content as compared to the wild type seeds can thus be identified and propagated.

To measure free amino acid composition of the seeds, free amino acids can be extracted from 8-10 milligrams of the seed meal in 1.0 mL of methanol/chloroform/water

mixed in ratio of 12v/5v/3v (MCW) at room temperature. The mixture can be vortexed and then centrifuged in an eppendorf microcentrifuge for about 3 min; approximately 0.8 mL of supernatant is then decanted. To this supernatant, 0.2 mL of chloroform is added followed by 0.3 mL of water. The mixture is then vortexed and centrifuged in an eppendorf microcentrifuge for about 3 min. The upper aqueous phase, approximately 1.0 mL, can then be removed and dried down in a Savant Speed Vac Concentrator. The samples are then hydrolyzed in 6N hydrochloric acid, 0.4% β-mercaptoethanol under nitrogen for 24 h at 110-120°C. Ten percent of the sample can then be analyzed using a Beckman Model 6300 amino acid analyzer using post-column ninhydrin detection. Relative free amino acid levels in the seeds are then compared as ratios of lysine, threonine, methionine, cysteine and/or isoleucine to leucine, thus using leucine as an internal standard.

EXAMPLE 11

Expression of Chimeric Genes in Microbial Cells

The cDNAs encoding the instant plant amino acid biosynthetic enzymes can be inserted into the T7 *E. coli* expression vector pET24d (Novagen). Plasmid DNA containing a cDNA may be appropriately digested to release a nucleic acid fragment encoding the enzyme. This fragment may then be purified on a 1% NuSieve GTG™ low melting agarose gel (FMC). Buffer and agarose contain 10 μg/ml ethidium bromide for visualization of the DNA fragment. The fragment can then be purified from the agarose gel by digestion with GELase™ (Epicentre Technologies) according to the manufacturer's instructions, ethanol precipitated, dried and resuspended in 20 μL of water. Appropriate oligonucleotide adapters may be ligated to the fragment using T4 DNA ligase (New England Biolabs, Beverly, MA). The fragment containing the ligated adapters can be purified from the excess adapters using low melting agarose as described above. The vector pET24d is digested, dephosphorylated with alkaline phosphatase (NEB) and deproteinized with phenol/chloroform as described above. The prepared vector pET24d and fragment can then be ligated at 16°C for 15 hours followed by transformation into DH5 electrocompetent cells (GIBCO BRL). Transformants can be selected on agar plates containing 2xYT media and 50 μg/mL kanamycin. Transformants containing gene enconding the enzyme are then screened for the correct orientation with respect to pET24d T7 promoter by restriction enzyme analysis.

Clones in the correct orientation with respect to the T7 promoter can be transformed into BL21(DE3) competent cells (Novagen) and selected on 2xYT agar plates containing 50 μg/ml kanamycin. A colony arising from this transformation construct can be grown overnight at 30°C in 2xYT media with 50 μg/mL kanamycin. The culture is then diluted two fold with fresh media, allowed to re-grow for 1 h, and induced by adding isopropyl-thiogalactopyranoside to 1 mM final concentration. Cells are then harvested by centrifugation after 3 h and re-suspended in 50 μL of 50 mM Tris-HCl at pH 8.0 containing 0.1 mM DTT and 0.2 mM phenyl methylsulfonyl fluoride. A small amount of 1 mm glass

beads can be added and the mixture sonicated 3 times for about 5 seconds each time with a microprobe sonicator. The mixture is centrifuged and the protein concentration of the supernatant determined. One μg of protein from the soluble fraction of the culture can be separated by SDS-polyacrylamide gel electrophoresis. Gels can be observed for protein bands migrating at the expected molecular weight.

EXAMPLE 12

Evaluating Compounds for Their Ability to Inhibit the Activity of a Plant Amino Acid Biosynthetic Enzyme

The plant amino acid biosynthetic enzymes described herein may be produced using any number of methods known to those skilled in the art. Such methods include, but are not limited to, expression in bacteria as described in Example 6, or expression in eukaryotic cell culture, *in planta*, and using viral expression systems in suitably infected organisms or cell lines. The instant enzymes may be expressed separately as mature proteins, or may be co-expressed in *E. coli* or another suitable expression background. In addition, whether expressed separately or in combination, the instant enzymes may be expressed either as mature forms of the proteins as observed *in vivo* or as fusion proteins by covalent attachment to a variety of enzymes, proteins or affinity tags. Common fusion protein partners include glutathione S-transferase ("GST"), thioredoxin ("Trx"), maltose binding protein, and C- and/or N-terminal hexahistidine polypeptide ("$(His)_6$"). The fusion proteins may be engineered with a protease recognition site at the fusion point so that fusion partners can be separated by protease digestion to yield intact mature enzymes. Examples of such proteases include thrombin, enterokinase and factor Xa. However, any protease can be used which specifically cleaves the peptide connecting the fusion protein and the biosynthetic enzyme.

Purification of the instant enzymes, if desired, may utilize any number of separation technologies familiar to those skilled in the art of protein purification. Examples of such methods include, but are not limited to, homogenization, filtration, centrifugation, heat denaturation, ammonium sulfate precipitation, desalting, pH precipitation, ion exchange chromatography, hydrophobic interaction chromatography and affinity chromatography, wherein the affinity ligand represents a substrate, substrate analog or inhibitor. When the enzymes are expressed as fusion proteins, the purification protocol may include the use of an affinity resin which is specific for the fusion protein tag attached to the expressed enzyme or an affinity resin containing ligands which are specific for the enzyme. For example, an enzyme may be expressed as a fusion protein coupled to the C-terminus of thioredoxin. In addition, a $(His)_6$ peptide may be engineered into the N-terminus of the fused thioredoxin moiety to afford additional opportunities for affinity purification. Other suitable affinity resins could be synthesized by linking the appropriate ligands to any suitable resin such as Sepharose-4B. In an alternate embodiment, a thioredoxin fusion protein may be eluted using dithiothreitol; however, elution may be accomplished using other reagents which interact to displace the thioredoxin from the resin. These reagents include β–mercaptoethanol or other

reduced thiol. The eluted fusion protein may be subjected to further purification by traditional means as stated above, if desired. Proteolytic cleavage of the thioredoxin fusion protein and the biosynthetic enzyme may be accomplished after the fusion protein is purified or while the protein is still bound to the ThioBond™ affinity resin or other resin.

Crude, partially purified or purified enzyme, either alone or as a fusion protein, may be utilized in assays for the evaluation of compounds for their ability to inhibit enzymatic activation of the plant amino acid biosynthetic enzymes disclosed herein. Assays may be conducted under well known experimental conditions which permit optimal enzymatic activity. Examples of assays for many of these enzymes can be found in *Methods in Enzymology* Vol. V, (Colowick and Kaplan eds.) Academic Press, New York or *Methods in Enzymology* Vol. XVII, (Tabor and Tabor eds.) Academic Press, New York. Specific examples may be found in the following references, each of which is incorporated herein by reference: dihydrodipicolinate reductase may be assayed as described in Farkas et al. (1965) *J. Biol. Chem. 240*: 4717-4722, or Cremer et al. (1988) *J. Gen. Microbiol. 134*:3221-3229; diaminopimelate epimerase may be assayed as described in Work (1962) in *Methods in Enzymology* Vol. V, (Colowick and Kaplan eds.) 858-864, Academic Press, New York; threonine synthase may be assayed as described in Giovanelli et al. (1984) *Plant Physiol 76*: 285-292 or Curien et al. (1996) *FEBS Lett. 390*: 85-90; threonine deaminase may be assayed as described in Tomova et al. (1968) *Biochemistry (USSR) 33*: 200-208 or Dougall (1970) *Phytochemistry 9*: 959-964; and S-adenosylmethionine synthetase may be assayed as described in Mudd (1960) *Biochim. Biophys.Acta 38*:354-355 or Boerjan et al. (1994) *Plant Cell 6*:1401-1414.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
(B) STREET: 1007 MARKET STREET
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(ii) TITLE OF INVENTION: PLANT AMINO ACID BIOSYNTHETIC ENZYMES

(iii) NUMBER OF SEQUENCES: 43

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: DISKETTE, 3.50 INCH
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
(D) SOFTWARE: MICROSOFT WORD VERSION 7.0A

(v) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/048,771
(B) FILING DATE: JUNE 6, 1997

(vii) ATTORNEY/AGENT INFORMATION:
(A) NAME: MAJARIAN, WILLIAM R.
(B) REGISTRATION NUMBER: 41,173
(C) REFERENCE/DOCKET NUMBER: BB-1087

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 908 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: csiln.pk0042.a3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ACGCGGGACA GATAAGTGGC ATGGACGAGC CGCTGGAGAT CCCTGTGCTG AACGACCTCA    60
CCATGGTTCT GGGCTCCATA GCGCAGTCGA GAGCAACCGG CGTGGTGGTC GACTTCAGCG   120
AGCCTTCAGC TGTTTACGAC AATGTCAAGC AGGCAGCGGC GTTTGGTCTG AGCAGCGTCG   180
TCTACGTTCC GAAAATCGAG CTAGAGACAG TGACTGAACT GTCAGCGTTC TGCGAGAAGG   240
CAAGCGGCTG CTTGGTTGCG CCAACGCTGT CGATTGGGTC CGTGCTCCTT CAGCAAGCGG   300
CTATACAGGC CTCGTTCCAC TACAGCAACG TTGAGATTGT GGAATCGAGA CCAAACCCAT   360
CGGATCTTCC ATCGCAAGAT GCAATCCAGA TTGCAAACAA CATATCAGAC CTTGGTCAGA   420
TATACAACAG GGAAGATATG GATTCCAGCA GTCCAGCCAG AGGCCAGCTG CTCGGGGAAG   480
ACGGAGTGCG CGTGCACAGC ATGGTTCTCC CTGGTCTCGT CTCCAGCACG TCGATCAACT   540
TCTCTGGCCC AGGAGAGATG TACACCTTAC GGCATGACGT TGCGAATGTT CAGTGCCTGA   600
TGCCAGGACT GATCCTGGCG ATACGGAAGG TGGTGCGGTT CAAGAACTTG ATTTATGGGC   660
TAGAGAAGTT CTTGTAGTGA ACAACAAACA ACCAATGCAA AACATCGACA GGCAACAGGC   720
AAGGCAGATA TCATCTGACG TCGCAACAAC CAAAACGACA GAGATTTGGA AAATAAAGGC   780
TGCACAGAAG ACGTCTGGGG TTTTGTGTGC ACCAGGCTGC GCAGAGAACG TCTGTCATTT   840
TGTGTGCACC ACTACGGCAC TACCTGCTGA GCGCGATTTT TATAAAAAAG GCATGGGAGG   900
GAGATCAT                                                            908
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: csiln.pk0042.a3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Ala Gly Gln Ile Ser Gly Met Asp Glu Pro Leu Glu Ile Pro Val Leu
1               5                   10                  15
```

```
Asn Asp Leu Thr Met Val Leu Gly Ser Ile Ala Gln Ser Arg Ala Thr
            20                  25                  30

Gly Val Val Val Asp Phe Ser Glu Pro Ser Ala Val Tyr Asp Asn Val
        35                  40                  45

Lys Gln Ala Ala Ala Phe Gly Leu Ser Ser Val Val Tyr Val Pro Lys
    50                  55                  60

Ile Glu Leu Glu Thr Val Thr Glu Leu Ser Ala Phe Cys Glu Lys Ala
65                  70                  75                  80

Ser Gly Cys Leu Val Ala Pro Thr Leu Ser Ile Gly Ser Val Leu Leu
                85                  90                  95

Gln Gln Ala Ala Ile Gln Ala Ser Phe His Tyr Ser Asn Val Glu Ile
            100                 105                 110

Val Glu Ser Arg Pro Asn Pro Ser Asp Leu Pro Ser Gln Asp Ala Ile
        115                 120                 125

Gln Ile Ala Asn Asn Ile Ser Asp Leu Gly Gln Ile Tyr Asn Arg Glu
    130                 135                 140

Asp Met Asp Ser Ser Ser Pro Ala Arg Gly Gln Leu Leu Gly Glu Asp
145                 150                 155                 160

Gly Val Arg Val His Ser Met Val Leu Pro Gly Leu Val Ser Ser Thr
                165                 170                 175

Ser Ile Asn Phe Ser Gly Pro Gly Glu Met Tyr Thr Leu Arg His Asp
            180                 185                 190

Val Ala Asn Val Gln Cys Leu Met Pro Gly Leu Ile Leu Ala Ile Arg
        195                 200                 205

Lys Val Val Arg Phe Lys Asn Leu Ile Tyr Gly Leu Glu Lys Phe Leu
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: rls2.pk0017.d3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
AAGATTGGCA GGAGAAATGC AGCAAAGGTC CTCTGCTCAA CGCAGATGCC GCCATCTCAG    60
AGCACAATCA AGGTTGTTAT CATTGGGGCG ACAAAAGAGA TTGGAAGAAC GGCAATAGCG   120
GCAGTAAGTA AAGCAAGGGG AATGGAGCTT GCAGGGGCCA TAGATTCTCA GTGTATAGGC   180
CTAGATGCAG GAGAGATAAG TGGCATGGGA AGAACCCTGG AAATTCCGGT GCTCAATGAT   240
CTCACAATGG TTCTGGGCTC AATTGCACAA ACCAGAGCAA CTGGAGTGGT GGTTGATTTT   300
AGTGAACCTT CAACTGTTTA TGATAATGTC AAACAGGCA                          339
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: rls2.pk0017.d3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Lys Ile Gly Arg Arg Asn Ala Ala Lys Val Leu Cys Ser Thr Gln Met
1               5                   10                  15

Pro Pro Ser Gln Ser Thr Ile Lys Val Val Ile Ile Gly Ala Thr Lys
            20                  25                  30

Glu Ile Gly Arg Thr Ala Ile Ala Ala Val Ser Lys Ala Arg Gly Met
        35                  40                  45

Glu Leu Ala Gly Ala Ile Asp Ser Gln Cys Ile Gly Leu Asp Ala Gly
    50                  55                  60

Glu Ile Ser Gly Met Gly Arg Thr Leu Glu Ile Pro Val Leu Asn Asp
65                  70                  75                  80

Leu Thr Met Val Leu Gly Ser Ile Ala Gln Thr Arg Ala Thr Gly Val
                85                  90                  95

Val Val Asp Phe Ser Glu Pro Ser Thr Val Tyr Asp Asn Val Lys Gln
            100                 105                 110

Ala
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Synechocystus sp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Ala Asn Gln Asp Leu Ile Pro Val Val Val Asn Gly Ala Ala Gly
1               5                   10                  15

Lys Met Gly Arg Glu Val Ile Lys Ala Val Ala Gln Ala Pro Asp Leu
            20                  25                  30

Gln Leu Val Gly Ala Val Asp His Asn Pro Ser Leu Gln Gly Gln Asp
        35                  40                  45

Ile Gly Glu Val Val Gly Ile Ala Pro Leu Glu Val Pro Val Leu Ala
    50                  55                  60
```

Asp Leu Gln Ser Val Leu Val Leu Ala Thr Gln Glu Lys Ile Gln Gly
65 70 75 80

Val Met Val Asp Phe Thr His Pro Ser Gly Val Tyr Asp Asn Val Arg
85 90 95

Ser Ala Ile Ala Tyr Gly Val Arg Pro Val Val Gly Thr Thr Gly Leu
100 105 110

Ser Glu Gln Gln Ile Gln Asp Leu Gly Asp Phe Ala Glu Lys Ala Ser
115 120 125

Thr Gly Cys Leu Ile Ala Pro Asn Phe Ala Ile Gly Val Leu Leu Met
130 135 140

Gln Gln Ala Ala Val Gln Ala Cys Gln Tyr Phe Asp His Val Glu Ile
145 150 155 160

Ile Glu Leu His His Asn Gln Lys Ala Asp Ala Pro Ser Gly Thr Ala
165 170 175

Ile Lys Thr Ala Gln Met Leu Ala Glu Met Gly Lys Thr Phe Asn Pro
180 185 190

Pro Ala Val Glu Glu Lys Glu Thr Ile Ala Gly Ala Lys Gly Gly Leu
195 200 205

Gly Pro Gly Gln Ile Pro Ile His Ser Ile Arg Leu Pro Gly Leu Ile
210 215 220

Ala His Gln Glu Val Leu Phe Gly Ser Pro Gly Gln Leu Tyr Thr Ile
225 230 235 240

Arg His Asp Thr Thr Asp Arg Ala Cys Tyr Met Pro Gly Val Leu Leu
245 250 255

Gly Ile Arg Lys Val Val Glu Leu Lys Gly Leu Val Tyr Gly Leu Glu
260 265 270

Lys Leu Leu
275

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1012 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: chp2.pk0008.h4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TATTGCCAGA GATGTGTGGT AATGGAGTCC GTTGCTTCGC TCGGTTTATA GCCGAGATTG 60

AAAATCTGCA GGGGACAAAT AGATTCACTA TTCATACTGG TGCTGGAAAG ATCGTTCCTG 120

AAATACAAAG TGATGGGCAG GTAAAGGTTG ATATGGGCGA GCCTATCCTT TCTGGACTAG 180

ACATCCCCAC AAAACTGCTA GCTACCAAGA ACAAAGCTGT TGTTCAAGCT GAATTGGCAG 240

TTGAGGGCTT AACATGGCAT GTCACATGTG TTAGCATGGG AAACCCTCAC TGTGTCACAT 300

```
TTGGTGCAAA TGAGTTAAAG GTATTGCAGG TCGACGATTT AAAACTTAGC GAAATTGGGC    360
CTAAATTTGA GCATCATGAA ATGTTTCCTG CTCGCACAAA CACAGAATTC GTACAGGTTT    420
TGTCTCGCTC ACACCTCAAA ATGCGGGTCT GGGAACGTGG TGCTGGAGCA ACTCTTGCCT    480
GTGGTACTGG TGCTTGTGCA GTGGTTGTTG CAGCTGTTCT TGAGGGTCGA GCTGAGCGGA    540
AATGTGTAGT TGATTTGCCT GGCGGGCCAT TGGAAATTGA GTGGAGGGAG GATGACAATC    600
ATGTTTACAT GACTGGTCCT GCAGAGGTCG TCTTTTATGG ATCTGTTGTT CACTAGGTAC    660
TGGGGACCAA GATAGAAGGG TTGGCTGCCA CTCAGAGCTT GTGAGATTGG TTATAGTATC    720
CATGAAACAG AGTGTTCTGG TACCAGTACA CTTGTTCAGA TATTCTTAAT TATGATTGCT    780
TGATTTGGGT AGCMGTAGAG GCTTCCTTTT GAAGCATTCT AGTGTTCMCC TTTTGTACTC    840
CTTTAGTTTG TCAGGTTTGA ACACTACATG GGTAACATGT CYTTCCCACC ATTTTCYGTT    900
TCTTTTCTTT GTAAGTGAAC GCCAATGCAG TTTTAGTATT GTTTTCTATA GATTTGTCTT    960
GATGCACTGG GCTTACTACT TATTTTCTGG TATGAATGCT GCCTATTTCC TG           1012
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: chp2.pk0008.h4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Leu Pro Glu Met Cys Gly Asn Gly Val Arg Cys Phe Ala Arg Phe Ile
1               5                   10                  15

Ala Glu Ile Glu Asn Leu Gln Gly Thr Asn Arg Phe Thr Ile His Thr
            20                  25                  30

Gly Ala Gly Lys Ile Val Pro Glu Ile Gln Ser Asp Gly Gln Val Lys
        35                  40                  45

Val Asp Met Gly Glu Pro Ile Leu Ser Gly Leu Asp Ile Pro Thr Lys
    50                  55                  60

Leu Leu Ala Thr Lys Asn Lys Ala Val Val Gln Ala Glu Leu Ala Val
65                  70                  75                  80

Glu Gly Leu Thr Trp His Val Thr Cys Val Ser Met Gly Asn Pro His
                85                  90                  95

Cys Val Thr Phe Gly Ala Asn Glu Leu Lys Val Leu Gln Val Asp Asp
            100                 105                 110

Leu Lys Leu Ser Glu Ile Gly Pro Lys Phe Glu His His Glu Met Phe
        115                 120                 125

Pro Ala Arg Thr Asn Thr Glu Phe Val Gln Val Leu Ser Arg Ser His
    130                 135                 140
```

Leu Lys Met Arg Val Trp Glu Arg Gly Ala Gly Ala Thr Leu Ala Cys
145 150 155 160

Gly Thr Gly Ala Cys Ala Val Val Val Ala Ala Val Leu Glu Gly Arg
165 170 175

Ala Glu Arg Lys Cys Val Val Asp Leu Pro Gly Gly Pro Leu Glu Ile
180 185 190

Glu Trp Arg Glu Asp Asp Asn His Val Tyr Met Thr Gly Pro Ala Glu
195 200 205

Val Val Phe Tyr Gly Ser Val Val His
210 215

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: rls48.pk0036.h10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTATCCGGC GCCGACGGTG TGATCTTCGT CATGCCGGGG GTCAATGGCG CGGACTACAC 60

CATGAGGATC TTCAACTCGG ACGGCAGTGA GCGGGAGATG TGTGGCAATG GAGTCCGTTG 120

CTTTGCCCGG TTTATAGCTG AGCTTGAAAA CCTACAGGGA ACACATAGCT TCAAAATTCA 180

CACTGGCGCT GGGCTAATCA TTCCTGAAAT ACAAAATGAT GGCAAGGTAA AGGTTGATAT 240

GGGCCAGCCC ATTCTCTCTG GACCAGATAT TCCAACAAAA CTGCCATCCA CCAAGAATGA 300

AGCCGTTGTC CAAGCTGATT TGGGCAGTTG ATGGCTCAAC ATGGCAAGTA ACCTGTGTTA 360

GCATGGGCAA TCCACATTGT GTCACATTTG GCACAAAGGA GCTCAAGGTT TTGCATGTTG 420

ATGATTAAAG CTTAATGATA TTGGGGCCTA AATTCAGCAT CATGAAATGT TCCTGCCCCA 480

C 481

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: rls48.pk0036.h10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Ser Gly Ala Asp Gly Val Ile Phe Val Met Pro Gly Val Asn Gly
1 5 10 15

```
Ala Asp Tyr Thr Met Arg Ile Phe Asn Ser Asp Gly Ser Glu Pro Glu
            20                  25                  30

Met Cys Gly Asn Gly Val Arg Cys Phe Ala Arg Phe Ile Ala Glu Leu
        35                  40                  45

Glu Asn Leu Gln Gly Thr His Ser Phe Lys Ile His Thr Gly Ala Gly
    50                  55                  60

Leu Ile Ile Pro Glu Ile Gln Asn Asp Gly Lys Val Lys Val Asp Met
65                  70                  75                  80

Gly Gln Pro Ile Leu
                85
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
ATCCCTTATT AAGCAGGGGT TTCGCGGCGC GAGACGGTGA CACTGGCAGA GTGGAATTTC     60

CGCCGCCATT CGAAGCTACA GCGATGGCCA TAACCGCCAC CATTTCCGTT CCCCTCACAT    120

CCCCCAGTCG CCGCACTCTC ACCTCCGTCA ATAGCCTCTC TCCCCTTTCT ACCCGATCCA    180

CTTTGCCCAC ACCGCAACGC ACTTTCAAAT ACCCTAATTC GCGCCTCGTC GTGTCTTCCA    240

TGAGCACCGA AACAGCCGTC AAAACTTCAT CCGCCTCCTT CCTCAACCGC AAGGAGTCCG    300

GCTTCCTCCA TTTCGCCAAG TACCACGGCC TCGGAAACGA CTTCGTTTTG ATTGACAATA    360

GAGACTCCTC CGAGCCCAAG ATCAGTGCTG AGAAAGCGGT GCAACTGTGT GATCGGAACT    420

TCGGCGTTGG AGCTGACGGA GTTATCTTTG TCTTGCCTGG CATCAGTGGC ACCGATTATA    480

CCATGAGGAT TTTTAACTCT GATGGTAGTG AGCCTGAGAT GTGTGGCAAT GGAGTTCGAT    540

GCTTTGCCAA ATTTGTTTCT CAGCTTGAGA ATTTACATGG GAGGCATAGT TTTACCATTC    600

ATACTGGTGC TGGTCTGATT ATTCCTGAAG TCTTGGAGGA TGGAAATGTC AGAGTTGATA    660

TGGGGGAGCC AGTTCTTAAA GCCTTGGATG TGCCTACTAA ATTACCTGCA AATAAGGATA    720

ATGCTGTTGT TAAATCACAG CTAGTTGTAG ATGGAGTTAT TTGGCATGTG ACCTGTGTTA    780

GCATGGGGAA TCCACACTGT GTAACTTTCA GTAGAGAAGG AAGCCAGAAT TTGCTTGTTG    840

ATGAATTGAA GCTAGCAGAA ATTGGGCCAA AATTTGAACA TCATGAGGTG TTCCCTGCAC    900

GAACTAACAC AGAGTTTGTG CAAGTATTAT CTAACTCTCA CTTGAAAATG CGTGTTTGGG    960

AGCGGGGAGC AGGAGCAACC CTAGCCTGTG GAACTGGAGC TTGTGCTACT GTTGTTGCAG   1020

CAGTTCTTGA GGGTCGTGCT GGGAGGAATT GCACGGTTGA TCTACCTGGA GGGCCTCTTC   1080

AGATTGAGTG GAGGGAGGAA GATAATCATG TTTATATGAC AGGCTCAGCC GATGTAGTTT   1140
```

ATTATGGTTC TTTGCCCCTT TGATATGTTG CCCCCATTGT TAAACCCAAT ATGGAATTAG 1200

GAATTGGTGA ATAATATTTG TATGAGAGGT GGACTTTCTG CTTGTTCCTA ATATTTTGCC 1260

ACGTCTTTAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A 1301

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
Met Ala Ile Thr Ala Thr Ile Ser Val Pro Leu Thr Ser Pro Ser Arg
1               5                   10                  15

Arg Thr Leu Thr Ser Val Asn Ser Leu Ser Pro Leu Ser Thr Arg Ser
            20                  25                  30

Thr Leu Pro Thr Pro Gln Arg Thr Phe Lys Tyr Pro Asn Ser Arg Leu
        35                  40                  45

Val Val Ser Ser Met Ser Thr Glu Thr Ala Val Lys Thr Ser Ser Ala
    50                  55                  60

Ser Phe Leu Asn Arg Lys Glu Ser Gly Phe Leu His Phe Ala Lys Tyr
65                  70                  75                  80

His Gly Leu Gly Asn Asp Phe Val Leu Ile Asp Asn Arg Asp Ser Ser
                85                  90                  95

Glu Pro Lys Ile Ser Ala Glu Lys Ala Val Gln Leu Cys Asp Arg Asn
            100                 105                 110

Phe Gly Val Gly Ala Asp Gly Val Ile Phe Val Leu Pro Gly Ile Ser
        115                 120                 125

Gly Thr Asp Tyr Thr Met Arg Ile Phe Asn Ser Asp Gly Ser Glu Pro
    130                 135                 140

Glu Met Cys Gly Asn Gly Val Arg Cys Phe Ala Lys Phe Val Ser Gln
145                 150                 155                 160

Leu Glu Asn Leu His Gly Arg His Ser Phe Thr Ile His Thr Gly Ala
                165                 170                 175

Gly Leu Ile Ile Pro Glu Val Leu Glu Asp Gly Asn Val Arg Val Asp
            180                 185                 190

Met Gly Glu Pro Val Leu Lys Ala Leu Asp Val Pro Thr Lys Leu Pro
        195                 200                 205

Ala Asn Lys Asp Asn Ala Val Val Lys Ser Gln Leu Val Val Asp Gly
    210                 215                 220

Val Ile Trp His Val Thr Cys Val Ser Met Gly Asn Pro His Cys Val
225                 230                 235                 240

Thr Phe Ser Arg Glu Gly Ser Gln Asn Leu Leu Val Asp Glu Leu Lys
                245                 250                 255
```

Leu Ala Glu Ile Gly Pro Lys Phe Glu His His Glu Val Phe Pro Ala
260 265 270

Arg Thr Asn Thr Glu Phe Val Gln Val Leu Ser Asn Ser His Leu Lys
275 280 285

Met Arg Val Trp Glu Arg Gly Ala Gly Ala Thr Leu Ala Cys Gly Thr
290 295 300

Gly Ala Cys Ala Thr Val Val Ala Ala Val Leu Glu Gly Arg Ala Gly
305 310 315 320

Arg Asn Cys Thr Val Asp Leu Pro Gly Gly Pro Leu Gln Ile Glu Trp
325 330 335

Arg Glu Glu Asp Asn His Val Tyr Met Thr Gly Ser Ala Asp Val Val
340 345 350

Tyr Tyr Gly Ser Leu Pro Leu
355

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: wlm24.pk0030.g4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCCACCGCC CCCTCCTCGG GCGGTCGCCT CCTCCGTCCG TTCTGTGGGA ATCCGCGCCC 60

CCGCCGCGCC GTCGCCTCGA TGGCCGTGTC CGCTCCCAAG TCGCCAGCCG CCGCCTCGTT 120

CCTCGAGCGC CGCGAGTCCG AGCGCGCGCT CCACTTCGTG AAGTACCAGG GCCTCGGCAA 180

CGACTTCATA ATGGTCGACA ACAGGGATTC GGCCGTACCG AAGGTGACAC CGGAGGAGGC 240

GGCGAAGCTA TGCGACCGAA ACTTTGGGTA TTGGGTGCTG ATGGCGTCAT CTTCGTCCTG 300

CCGGGGGTCA ACGGCGCGGA CTACACTATG AGGATATTCA ACTCCGATGG CAGCAACCGG 360

AATGTNTGGN ATGGATTCGT TGCTTGCTCG CTTTATACGG AGTTGAAATC TACANGGAAA 420

CATACTTCAA AACAANAGGG GGCTGGATTA ATATCCTGAA ATANANACAT GNAAGTTANG 480

TNATATGGGC AACAATCTTA TGGCANATTT CANAAAATGC ATCACAAGAT AACTTNTAAA 540

ACGATTGAAT TAGGCAANAG AANTACCGTT ATAGGAACCC ATGAANCTTG TNAAATTAAG 600

GT 602

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: wlm24.pk0030.g4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Ala Leu His Phe Val Lys Tyr Gln Gly Leu Gly Asn Asp Phe Ile Met
1               5                   10                  15

Val Asp Asn Arg Asp Ser Ala Val Pro Lys Val Thr Pro Glu Glu Ala
            20                  25                  30

Ala Lys Leu Cys Asp Arg Asn Phe Gly Xaa Gly Ala Asp Gly Val Ile
        35                  40                  45

Phe Val Leu Pro Gly Val Asn Gly Ala Asp Tyr Thr Met Arg Ile Phe
    50                  55                  60

Asn Ser Asp Gly Ser Asn Arg Asn Val Trp Xaa Gly Phe Val Ala Cys
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Synechocystus sp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Ala Leu Ser Phe Ser Lys Tyr His Gly Leu Gly Asn Asp Phe Ile
1               5                   10                  15

Leu Val Asp Asn Arg Gln Ser Thr Glu Pro Cys Leu Thr Pro Asp Gln
            20                  25                  30

Ala Gln Gln Leu Cys Asp Arg His Phe Gly Ile Gly Ala Asp Gly Val
        35                  40                  45

Ile Phe Ala Leu Pro Gly Gln Gly Gly Thr Asp Tyr Thr Met Arg Ile
    50                  55                  60

Phe Asn Ser Asp Gly Ser Glu Pro Glu Met Cys Gly Asn Gly Ile Arg
65                  70                  75                  80

Cys Leu Ala Lys Phe Leu Ala Asp Leu Glu Gly Val Glu Glu Lys Thr
                85                  90                  95

Tyr Arg Ile His Thr Leu Ala Gly Val Ile Thr Pro Gln Leu Leu Ala
            100                 105                 110

Asp Gly Gln Val Lys Val Asp Met Gly Glu Pro Gln Leu Leu Ala Glu
        115                 120                 125

Leu Ile Pro Thr Thr Leu Ala Pro Ala Gly Glu Lys Val Val Asp Leu
    130                 135                 140

Pro Leu Ala Val Ala Gly Gln Thr Trp Ala Val Thr Cys Val Ser Met
145                 150                 155                 160
```

```
Gly Asn Pro His Cys Leu Thr Phe Val Asp Asp Val Asp Ser Leu Asn
                165                 170                 175

Leu Thr Glu Ile Gly Pro Leu Phe Glu His His Pro Gln Phe Ser Gln
            180                 185                 190

Arg Thr Asn Thr Glu Phe Ile Gln Val Leu Gly Ser Asp Arg Leu Lys
        195                 200                 205

Met Arg Val Trp Glu Arg Gly Ala Gly Ile Thr Leu Ala Cys Gly Thr
    210                 215                 220

Gly Ala Cys Ala Thr Val Val Ala Ala Val Leu Thr Gly Arg Gly Asp
225                 230                 235                 240

Arg Arg Cys Thr Val Glu Leu Pro Gly Gly Asn Leu Glu Ile Glu Trp
                245                 250                 255

Ser Ala Gln Asp Asn Arg Leu Tyr Met Thr Gly Pro Ala Gln Arg Val
            260                 265                 270

Phe Ser Gly Gln Ala Glu Ile
        275
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: cc2.pk0031.c9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
GTCGGCTGCG CGTCCACGGG AGACACCTCC GCCGCGCTCT CGGCCTACTG CGCAGCCGCG     60

GGAATCCCCG CCATCGTGTT CCTGCCAGCG GACCGCATCT CGCTGCAGCA GCTCATCCAG    120

CCGATCGCCA ACGGCGCCAC CGTGCTCTCT CTAGACACTG ATTTTGATGG CTGCATGCGG    180

CTCATTCGCG AGGTCACTGC AGAGCTGCCA ATCTACCTTG CCAATTCGCT CAACCCGCTC    240

CGCCTTGAGG GGCAGAAGAC AGCGGCCATC GAGATATTGC AGCAGTTCAA TTGGCAGGTG    300

CCAGATTGGG TCATTGTTCC AGGAGGCAAT CTTGGGAATA TCTATGCATT CTACAAGGGG    360

TTTGAGATGT GCCGCGTTCT TGGACTTGTT GATCGCGTGC CACGGCTTGT CTGCGCACAG    420

GCTGCAAATG CAAATCCATT GTACCGGTAC TACAAGTCAG GTTGGACTGA GTTTGAGCCA    480

CAAACTGCCG AGACTACATT TGCATCTGCG ATACAGATTG GTGATCCTGT ATCTGTTGAC    540

CGTGCGGTGG TCGCGCTGAA GGCCACTGAC GGTATTGTGG AGGAGGCTAC AGAGGAGGAG    600

CTAATGGATG CAACGGCGCT TGCTGACCGC ACTGGGATGT TTGCTTGCCC ACATACTGGG    660

GTTGCACTTG CTGCTTTGTT TAAGCTTCAG GGTCAGCGTA TAATTGGCCC TAATGACCGC    720

ACTGTGGTTG TTAGCACAGC TCATGGGCTG AAGTTCACGC AGTCAAAGAT TGACTACCAT    780
```

GACAAAAACA TCAAAGACAT GGTTTGCCAG TATGCTAATC CACCGATCAG TGTGAAGGCT 840

GACTTTGGTT CTGTGATGGA TGTTCTCCAG AAAAATCTCA ATGGTAAGAT ATAAAGTTAT 900

ATGATTAATT AACCCTCCAA ACTGTTTTTT TTTGTTTTTT CGTTCCAGGA ATTTTATTCC 960

TGAGTCTTTC AACTTTGTTT GGTGAACATG GTATGGTGCT AAAATCTAGA CCTAATACCT 1020

TGTAGTACTA GTTCTGGAGG CTCTTTTGGT TGTAGGTCGA AGTGGATAGA GCTGTTCCTT 1080

GTACTTTATC TGTTTCATGT AATATGAATA ATAAATTATG GTCTAAATAT TTGAATAAAA 1140

AATCGTTTGG AATGACCCAC 1160

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: cc2.pk0031.c9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Gly Cys Ala Ser Thr Gly Asp Thr Ser Ala Ala Leu Ser Ala Tyr
1 5 10 15

Cys Ala Ala Ala Gly Ile Pro Ala Ile Val Phe Leu Pro Ala Asp Arg
20 25 30

Ile Ser Leu Gln Gln Leu Ile Gln Pro Ile Ala Asn Gly Ala Thr Val
35 40 45

Leu Ser Leu Asp Thr Asp Phe Asp Gly Cys Met Arg Leu Ile Arg Glu
50 55 60

Val Thr Ala Glu Leu Pro Ile Tyr Leu Ala Asn Ser Leu Asn Pro Leu
65 70 75 80

Arg Leu Glu Gly Gln Lys Thr Ala Ala Ile Glu Ile Leu Gln Gln Phe
85 90 95

Asn Trp Gln Val Pro Asp Trp Val Ile Val Pro Gly Gly Asn Leu Gly
100 105 110

Asn Ile Tyr Ala Phe Tyr Lys Gly Phe Glu Met Cys Arg Val Leu Gly
115 120 125

Leu Val Asp Arg Val Pro Arg Leu Val Cys Ala Gln Ala Ala Asn Ala
130 135 140

Asn Pro Leu Tyr Arg Tyr Tyr Lys Ser Gly Trp Thr Glu Phe Glu Pro
145 150 155 160

Gln Thr Ala Glu Thr Thr Phe Ala Ser Ala Ile Gln Ile Gly Asp Pro
165 170 175

Val Ser Val Asp Arg Ala Val Val Ala Leu Lys Ala Thr Asp Gly Ile
180 185 190

```
Val Glu Glu Ala Thr Glu Glu Glu Leu Met Asp Ala Thr Ala Leu Ala
        195                 200                 205

Asp Arg Thr Gly Met Phe Ala Cys Pro His Thr Gly Val Ala Leu Ala
    210                 215                 220

Ala Leu Phe Lys Leu Gln Gly Gln Arg Ile Ile Gly Pro Asn Asp Arg
225                 230                 235                 240

Thr Val Val Val Ser Thr Ala His Gly Leu Lys Phe Thr Gln Ser Lys
                245                 250                 255

Ile Asp Tyr His Asp Lys Asn Ile Lys Asp Met Val Cys Gln Tyr Ala
            260                 265                 270

Asn Pro Pro Ile Ser Val Lys Ala Asp Phe Gly Ser Val Met Asp Val
        275                 280                 285

Leu Gln Lys Asn Leu Asn Gly Lys Ile
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: csl.pk0058.g5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
ATGGCTTGCA AGTACTCCAA CCCGCCTGTG AGCGTGAAGG CTGACTTTGG CGCCGTGATG    60

GATGTGCTGA AGAAGAGGCT CAAGGGCAAG CTCTGAGCGC CTGTGCCTGG CTAATGCAAT   120

CAACTGATTG GAATGCAGTG GTTTCGTCGG TATCGGGGGG TCTTTTAGGC TTCAGAAATT   180

CTGTCTGGGT TAGACTATTT GTTTGTGGAG TTTAGCAGGA GAATGGCTAT CTCTCCTGCA   240

AGACTGGCGC TCTTTCTTGT GCTACGAATG TGTTACCATG GATAATAAGT GTAGTCGCTG   300

TCGGATTGAA TAATCAAAAA AAAAN                                         325
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: csl,pk0058.g5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Met Ala Cys Lys Tyr Ser Asn Pro Pro Val Ser Val Lys Ala Asp Phe
1               5                   10                  15
```

Gly Ala Val Met Asp Val Leu Lys Lys Arg Leu Lys Gly Lys Leu
20 25 30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: rls72.pk0018.e7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
ACACCCAACA CGCAGACTTG ACAGATTCTG CTACTACAAA TCCTGCATAT TTAACAGCGC    60
TGCAACTCGA CGATGGAGAA CGGTGCTGCA ACCAACGGGG CGTCGGAGAA GTCGCACTCT   120
CCTTCACAGA CCTACCTCTC CACAAGGGGA GACGATTATG GGCTCTCATT CGAGACCGTC   180
GTCCTCAAAG GTCTTGCGGC TGACGGGGGT CTTTTCCTGC CCGAGGAAGT GCCCCGCGGCA  240
ACCGAGTGGC AAAGCTGGAA AGACCTGCCC TACACCGAGC TTGCCGTCAA GGTTCTCAGC   300
TTGTACATCT CCCCCGCCGA GGTGCCGACG GAAGACCTCA GGGCGCTCGT CGAGCGCAGC   360
TACTCGACCT TCCGATCCAA GGAGGTTGTG CCGCTGGTGA AGCTGGAGGA CAACCTTCAC   420
CTGCTGGAGC TATTCCACGG CCCCAACTAC TCGTTCAAGG ACTGCGCGCT GCAATTCCTT   480
GGTAACCTCN TCGAGTACTT TTGACTCNCA AGAACAAGGG AAAGGAGG                528
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: rls72.pk0018.e7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Glu Asn Gly Ala Ala Thr Asn Gly Ala Ser Glu Lys Ser His Ser
1 5 10 15

Pro Ser Gln Thr Tyr Leu Ser Thr Arg Gly Asp Asp Tyr Gly Leu Ser
20 25 30

Phe Glu Thr Val Val Leu Lys Gly Leu Ala Ala Asp Gly Gly Leu Phe
35 40 45

Leu Pro Glu Glu Val Pro Ala Ala Thr Glu Trp Gln Ser Trp Lys Asp
50 55 60

Leu Pro Tyr Thr Glu Leu Ala Val Lys Val Leu Ser Leu Tyr Ile Ser
65 70 75 80

Pro Ala Glu Val Pro Thr Glu Asp Leu Arg Ala Leu Val Glu Arg Ser
85 90 95

Tyr Ser Thr Phe Arg Ser Lys Glu Val Val Pro Leu Val Lys Leu Glu
100 105 110

Asp Asn Leu His Leu Leu Glu Leu Phe His Gly Pro Asn Tyr Ser Phe
115 120 125

Lys Asp Cys Ala Leu Gln Phe Leu Gly Asn Leu Xaa Glu Tyr Phe
130 135 140

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: sel.06a03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATGCAATG GTGCAGGCTG ATTCCACTGG AATGTTCATA TGTCCACACA CTGGGGTGGC 60

TCTGGCGGCG CTTATTAAGC TGAGGAATCG TGGGGTTATC GGTGCCGGTG AGAGGGTTGT 120

GGTGGTGAGC ACTGCACATG GATTGAAGTT TGCACAGAGC AAGATTGATT ATCATTCTGG 180

GCTCATTCCT GGAATGGGCC GCTATGCTAA CCCGCTGGTT TCGGTTAAGG CGGATTTTGG 240

ATCGGTCATG GATGTTCTCA AGGATTCTTG CACAACAAGT CCCCCGACTT TAACAAGTCT 300

TGACGTTGCC AAGTAAGTTT TAGTTCGGGG TTTTTTCTGA TTAAAGATGT TTTTAAACAT 360

GTTTGTGTNC ACTTTCGGTC GTTATTATGG ATTTGTAAGA TTGGGCCCAA GTATTCGAGG 420

GTTTGATTTC AAACAACATG CTTCTGGTGA CGCAATGCAA ATTTCGGNGC ATAACATCAT 480

TGTCGAAGAT GGATCNCGAC CGATGAAACT GTGTGGCAAG TAATGAGAAG AAAATAGGGC 540

ACTTGTACAG AGATTTNAAA GNTTAATTTC N 571

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: sel.06a03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asp Ala Met Val Gln Ala Asp Ser Thr Gly Met Phe Ile Cys Pro His
1 5 10 15

Thr Gly Val Ala Leu Ala Ala Leu Ile Lys Leu Arg Asn Arg Gly Val
20 25 30

Ile Gly Ala Gly Glu Arg Val Val Val Val Ser Thr Ala His Gly Leu
35 40 45

Lys Phe Ala Gln Ser Lys Ile Asp Tyr His Ser Gly Leu Ile Pro Gly
50 55 60

Met Gly Arg Tyr Ala Asn Pro Leu Val Ser Val Lys Ala Asp Phe Gly
65 70 75 80

Ser Val Met Asp Val Leu Lys Asp Ser Cys Thr Thr Ser Pro Pro Thr
85 90 95

Leu Thr Ser Leu Asp Val Ala Lys
100

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: srl.pk0003.f6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTTCCTCTT CTCTGTTTCA GTCTCTCCCT TTCTCTCTCC AAACCTCTAA ACCCTACGCG 60

CCTCCCAAAC CCGCCGCCCA CTTCGTTGTC CGCGCCCAAT CCCCCCTCAC TCAGAACAAC 120

AACTCCTCCT CCAAGCATCG CCGCCCCGCC GACGAGAACA TCCGCGACGA GGCCCGCCGC 180

ATCAATGCGC CCCACGACCA CCACCTCTTC TCGGCCAAGT ACGTCCCCTT CAACGCCGAC 240

TCCTCCTCCT CCTCCTCCAC GGAGTCCTAC TCGCTCGACG AGATCGTCTA CCGCTCCCAA 300

TCCGGCGGCC TCCTGGACGT CCAGCACGAC ATGGATGCCC TCAAGCGTTT CGACGGCGAG 360

TACTGGCGCA ACCTCTTCGA CTCGCGCGTG GGCAAAACCA CCTGGCCTTA CGGCTCCGGC 420

GTCTGGAGCA AAAAAGAATG GGTCCTCCCC GAGATCCACG ACGACGATAT CGTCTCCGCC 480

TTCGAGGGTA ACTCCAACCT CTTCTGGGCC GAGCGTTTCG GCAAACAGTT CCTCGGCATG 540

AACGATTTGT GGGTCAAACA CTGCGGAATC AGCCACACGG GCAGCTTCAA GGATCTCGGC 600

ATGACCGTCC TCGTCAGCCA GGTCAATCGC TTGAGAAAAA TGAACCGCCC CGTCGTCGGT 660

GTTGGTTGCG CCTCCACCGG TGACACATCG GCCGCTTTAT CCGCCTATTG CGCTTCCGCT 720

GCCATTCCTT CCATTGTGTT TTTGCCTGCT AATAAAATCT CTCTTGCCCA ACTTGTTCAG 780

CCTATTGCCA ATGGAGCCTT TGTGTTGAGT ATCGACACTG ATTTTGATGG TTGCATGCAG 840

TTGATCAGAG AAGTCACTGC TGAATTGCCT ATTTATTTGG CTAACTCTCT CAACAGTTTG 900

AAGTTGGAAG GGCAGAAAAC TGCTGCTATT GAGATTCTGC AGCAGTTTGA TTGGCAGGTT 960

CCTGATTGGG TCATTGTGCC TGGAAGCAAC CTTGGCAACA TTTATGCCTT TTACAAAGGG 1020

TTTAAGATGT TTCAAGAGCT TGGGCTTGTG GATAAGATTC CAAGGCTTGT TTGTGCTCAG 1080

GCTGCCAATG CTGATCCTTT GTATTTGTAC TTTAAATCCG GGTGGAAGGA GTTTAAGCCT 1140

GTGAAGTCGA GCACTACATT TGCTTCTGCC ATTCAAATTG GTGATCCTGT TTCCATTGAC 1200

AGGGCGGTTC ACGCGCTAAA GAGTTGCGAT GGGATTGTGG AGGAGGCCAC GGAGGAGGAG 1260

TTGATGGATG CTACAGCGCA GGCGGATTCT ACTGGGATGT TTATTTGCCC CCACACCGGG 1320

GTTGCTTTAA CTGCATTGTT TAAGCTCAGG AACAGCGGGG TTATTAAGGC CACTGATAGG 1380

ACTGTGGTGG TTAGCACTGC TCATGGCTTG AAGTTCACTC AGTCCAAGAT TGATTACCAT 1440

TCTAAGGACA TCAAGGACAT GGCTTGCCGC TATGCTAACC CGCCCATGCA AGTGAAGGCA 1500

GACTTTGGCT CGGTTATGGA TGTTTTGAAG ACGTATTTGC AGAGTAAGGC TCATTAGGTT 1560

AGCATTGCAA GTTTTGCTCC TCCTGAGTTT GCTCATTATT TACTTACTTT TAGGCACTAC 1620

TGCTGTATTG TCTTTTCTAT GAGCTAGGTT TGAGTGTTGT AATAATTTGC TTGCTGCATT 1680

ATGTATGCCG TCTAGTGTTC CATATTGGGC ATCATCCTTA GTATTTGTTG TAGATTTTCT 1740

TTGCTGAGCA TTTGATATAA TAGCTCAAGT AGGAAAATGA ATTGGGTACT ATGAGGAATG 1800

CATATCATTG GCTTGTTATT ACTGGATTCC AGACCACCCC AAAAGAAAAT AATTCCAAAA 1860

AATATAATTA GAACAAATTT CGTCCTTGTT ATGCTGTTGG CATTAAGCTC AGTGTGGGTA 1920

TTACCAAGCA ACTCGAAATC AAGAGAAAAA AAAATTGACA GCAAAGGAGC TGCATTGTTG 1980

GACTGAGTCA CATCACTTCA TTGCTATGTC GTCATATTTC GTTGAATTAC GGGAAGGCAG 2040

CATGCACAGC AATATGCAGC GATTAACTGA AGCCACACCG CACACATTGA AGTAGTAGTC 2100

AATTTAGACA CTCCATCTTG TACTTTCTAC AAAAATGAAT TTTTCTTAGC CATTAAGTAT 2160

AATATTTTAT TCTAAAAAAA AAAAAAAAAA A 2191

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 518 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: srl.pk0003.f6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ala Ser Ser Ser Leu Phe Gln Ser Leu Pro Phe Ser Leu Gln Thr Ser
1 5 10 15

Lys Pro Tyr Ala Pro Pro Lys Pro Ala Ala His Phe Val Val Arg Ala
20 25 30

Gln Ser Pro Leu Thr Gln Asn Asn Asn Ser Ser Ser Lys His Arg Arg
35 40 45

```
Pro Ala Asp Glu Asn Ile Arg Asp Glu Ala Arg Arg Ile Asn Ala Pro
    50                  55                  60

His Asp His His Leu Phe Ser Ala Lys Tyr Val Pro Phe Asn Ala Asp
65                  70                  75                  80

Ser Ser Ser Ser Ser Ser Thr Glu Ser Tyr Ser Leu Asp Glu Ile Val
                85                  90                  95

Tyr Arg Ser Gln Ser Gly Gly Leu Leu Asp Val Gln His Asp Met Asp
            100                 105                 110

Ala Leu Lys Arg Phe Asp Gly Glu Tyr Trp Arg Asn Leu Phe Asp Ser
        115                 120                 125

Arg Val Gly Lys Thr Thr Trp Pro Tyr Gly Ser Gly Val Trp Ser Lys
    130                 135                 140

Lys Glu Trp Val Leu Pro Glu Ile His Asp Asp Asp Ile Val Ser Ala
145                 150                 155                 160

Phe Glu Gly Asn Ser Asn Leu Phe Trp Ala Glu Arg Phe Gly Lys Gln
                165                 170                 175

Phe Leu Gly Met Asn Asp Leu Trp Val Lys His Cys Gly Ile Ser His
            180                 185                 190

Thr Gly Ser Phe Lys Asp Leu Gly Met Thr Val Leu Val Ser Gln Val
        195                 200                 205

Asn Arg Leu Arg Lys Met Asn Arg Pro Val Val Gly Val Gly Cys Ala
    210                 215                 220

Ser Thr Gly Asp Thr Ser Ala Ala Leu Ser Ala Tyr Cys Ala Ser Ala
225                 230                 235                 240

Ala Ile Pro Ser Ile Val Phe Leu Pro Ala Asn Lys Ile Ser Leu Ala
                245                 250                 255

Gln Leu Val Gln Pro Ile Ala Asn Gly Ala Phe Val Leu Ser Ile Asp
            260                 265                 270

Thr Asp Phe Asp Gly Cys Met Gln Leu Ile Arg Glu Val Thr Ala Glu
        275                 280                 285

Leu Pro Ile Tyr Leu Ala Asn Ser Leu Asn Ser Leu Lys Leu Glu Gly
    290                 295                 300

Gln Lys Thr Ala Ala Ile Glu Ile Leu Gln Gln Phe Asp Trp Gln Val
305                 310                 315                 320

Pro Asp Trp Val Ile Val Pro Gly Ser Asn Leu Gly Asn Ile Tyr Ala
                325                 330                 335

Phe Tyr Lys Gly Phe Lys Met Phe Gln Glu Leu Gly Leu Val Asp Lys
            340                 345                 350

Ile Pro Arg Leu Val Cys Ala Gln Ala Ala Asn Ala Asp Pro Leu Tyr
        355                 360                 365

Leu Tyr Phe Lys Ser Gly Trp Lys Glu Phe Lys Pro Val Lys Ser Ser
    370                 375                 380

Thr Thr Phe Ala Ser Ala Ile Gln Ile Gly Asp Pro Val Ser Ile Asp
385                 390                 395                 400
```

```
Arg Ala Val His Ala Leu Lys Ser Cys Asp Gly Ile Val Glu Glu Ala
                405                 410                 415

Thr Glu Glu Glu Leu Met Asp Ala Thr Ala Gln Ala Asp Ser Thr Gly
            420                 425                 430

Met Phe Ile Cys Pro His Thr Gly Val Ala Leu Thr Ala Leu Phe Lys
        435                 440                 445

Leu Arg Asn Ser Gly Val Ile Lys Ala Thr Asp Arg Thr Val Val Val
    450                 455                 460

Ser Thr Ala His Gly Leu Lys Phe Thr Gln Ser Lys Ile Asp Tyr His
465                 470                 475                 480

Ser Lys Asp Ile Lys Asp Met Ala Cys Arg Tyr Ala Asn Pro Pro Met
                485                 490                 495

Gln Val Lys Ala Asp Phe Gly Ser Val Met Asp Val Leu Lys Thr Tyr
            500                 505                 510

Leu Gln Ser Lys Ala His
        515
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 643 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: wr1.pk0085.h2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
GCTCATCCAG CCCATCGCCA ACGGCGCCAC GGTGCTCTCG CTTGACACGG ATTTCGACGG     60

ATGCATGCGG CTTATCAGGG AGGTGACAGC TGAGCTGCCC ATATACCTCG CAAACTCACT    120

CAACTCGCTT CCGGCTGGAG GGGCAGAAGA CTGCAGCCAT CCGAGATATT GCAACANTCA    180

ATTGGCAGGT GCCCGGACTG GGTCACATCC CAAGGAGGCA ATCTGGGGGA ACATTTTATG    240

CTTTCCTACA AGGATTTNAA TTTCCGTGTC CTTNGCTAGT TGATTNCCTT CCNACTCCTT    300

GTTANTNCAA NAGGCCGCCA ACGCAAACCC ACTGTACCCG TACTACAATC CTGGGGTGAC    360

TGATTTCCAT CCACTTGNTT GCCGGGACAA TTTNCATCCN GCAACAATTT GGGGATTCCA    420

TATCNATTAC CNTCGGTTTT TTCNCCCTNA AAGGACNNAT GATTNTCCNA GGAACTCCNN    480

AGGNGGATCA AGGATCCAAA GGCTTTCTAC TCACTGGAAN TTGCTTCCCA ANACGGGGTT    540

CACTNCCGCC CGTTAAACCC NTGACAAGTA TAATGGACAA CACNCCGGGG TNTATNACAA    600

CGGCAANTTN AAANCAAGTT NATCATTAGA ACNGGAANTT NCC                      643
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: wrl.pk0085.h2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Ile Gln Pro Ile Ala Asn Gly Ala Thr Val Leu Ser Leu Asp Thr
1 5 10 15

Asp Phe Asp Gly Cys Met Arg Leu Ile Arg Glu Val Thr Ala Glu Leu
20 25 30

Pro Ile Tyr Leu Ala Asn Ser Leu Asn Ser Leu Xaa Leu Glu Gly Gln
35 40 45

Lys Thr Ala Ala Ile Arg Asp Ile Ala Thr Xaa Asn Trp Gln Val Pro
50 55 60

Gly Leu Gly His Ile Pro Arg Arg Gln Ser Xaa Thr Phe Tyr Ala Phe
65 70 75 80

Leu Gln Gly Phe

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 525 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Arabidopsis thaliana

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Ser Ser Cys Leu Phe Asn Ala Ser Val Ser Ser Leu Asn Pro Lys
1 5 10 15

Gln Asp Pro Ile Arg Arg His Arg Ser Thr Ser Leu Leu Arg His Arg
20 25 30

Pro Val Val Ile Ser Cys Thr Ala Asp Gly Asn Asn Ile Lys Ala Pro
35 40 45

Ile Glu Thr Ala Val Lys Pro Pro His Arg Thr Glu Asp Asn Ile Arg
50 55 60

Asp Glu Ala Arg Arg Asn Arg Ser Asn Ala Val Asn Pro Phe Ser Ala
65 70 75 80

Lys Tyr Val Pro Phe Asn Ala Ala Pro Gly Ser Thr Glu Ser Tyr Ser
85 90 95

Leu Asp Glu Ile Val Tyr Arg Ser Arg Ser Gly Gly Leu Leu Asp Val
100 105 110

Glu His Asp Met Glu Ala Leu Lys Arg Phe Asp Gly Ala Tyr Trp Arg
115 120 125

```
Asp Leu Phe Asp Ser Arg Val Gly Lys Ser Thr Trp Pro Tyr Gly Ser
    130                 135                 140

Gly Val Trp Ser Lys Lys Glu Trp Val Leu Pro Glu Ile Asp Asp Asp
145                 150                 155                 160

Asp Ile Val Ser Ala Phe Glu Gly Asn Ser Asn Leu Phe Trp Ala Glu
                165                 170                 175

Arg Phe Gly Lys Gln Phe Leu Gly Met Asn Asp Leu Trp Val Lys His
            180                 185                 190

Cys Gly Ile Ser His Thr Gly Ser Phe Lys Asp Leu Gly Met Thr Val
        195                 200                 205

Leu Val Ser Gln Val Asn Arg Leu Arg Lys Met Lys Arg Pro Val Val
    210                 215                 220

Gly Val Gly Cys Ala Ser Thr Gly Asp Thr Ser Ala Ala Leu Ser Ala
225                 230                 235                 240

Tyr Cys Ala Ser Ala Gly Ile Pro Ser Ile Val Phe Leu Pro Ala Asn
                245                 250                 255

Lys Ile Ser Met Ala Gln Leu Val Gln Pro Ile Ala Asn Gly Ala Phe
            260                 265                 270

Val Leu Ser Ile Asp Thr Asp Phe Asp Gly Cys Met Lys Leu Ile Arg
        275                 280                 285

Glu Ile Thr Ala Glu Leu Pro Ile Tyr Leu Ala Asn Ser Leu Asn Ser
    290                 295                 300

Leu Arg Leu Glu Gly Gln Lys Thr Ala Ala Ile Glu Ile Leu Gln Gln
305                 310                 315                 320

Phe Asp Trp Gln Val Pro Asp Trp Val Ile Val Pro Gly Gly Asn Leu
                325                 330                 335

Gly Asn Ile Tyr Ala Phe Tyr Lys Gly Phe Lys Met Cys Gln Glu Leu
            340                 345                 350

Gly Leu Val Asp Arg Ile Pro Arg Met Val Cys Ala Gln Ala Ala Asn
        355                 360                 365

Ala Asn Pro Leu Tyr Leu His Tyr Lys Ser Gly Trp Lys Asp Phe Lys
    370                 375                 380

Pro Met Thr Ala Ser Thr Thr Phe Ala Ser Ala Ile Gln Ile Gly Asp
385                 390                 395                 400

Pro Val Ser Ile Asp Arg Ala Val Tyr Ala Leu Lys Lys Cys Asn Gly
                405                 410                 415

Ile Val Glu Glu Ala Thr Glu Glu Glu Leu Met Asp Ala Met Ala Gln
            420                 425                 430

Ala Asp Ser Thr Gly Met Phe Ile Cys Pro His Thr Gly Val Ala Leu
        435                 440                 445

Thr Ala Leu Phe Lys Leu Arg Asn Gln Gly Val Ile Ala Pro Thr Asp
    450                 455                 460

Arg Thr Val Val Val Ser Thr Ala His Gly Leu Lys Phe Thr Gln Ser
465                 470                 475                 480
```

Lys Ile Asp Tyr His Ser Asn Ala Ile Pro Asp Met Ala Cys Arg Phe
485 490 495

Ser Asn Pro Pro Val Asp Val Lys Ala Asp Phe Gly Ala Val Met Asp
500 505 510

Val Leu Lys Ser Tyr Leu Gly Ser Asn Thr Leu Thr Ser
515 520 525

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: cen1.pk0064.f4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAACAGTGGT CCTTGAGGGG GACTCATATG ATGAAGCTCA GTCATATGCA AAATTGCGTT 60

GCCAGCAGGA AGGCCGCACA TTTGTACCTC CTTTTGACCA TCCTGATGTC ATCACTGGAC 120

AAGGAACTAT CGGCATGGAA ATTGTTAGGC AGCTGCAAGG TCCACTGCAT GCAATATTTG 180

TACCTGTTGG AGGTGGTGGA TTAATTGCTG GAATTGCTGC CTATGTAAAA CGGGTTCGCC 240

CAGAGGTGAA AATAATTGGA GTGGAACCCT CAGATGCAAA TGCAATGGCA TTATCCTTGT 300

GTCATGGTAA GAGGGTCATG TTGGAGCATG TTGGTGGGTT TGCTGATGGT GTAGCTGTCA 360

AAGCTGTTGG GGAAGAAACA TTTCGCCTGT GCAGAGAGCT AGTAGATGGC ATTGTTATGG 420

TCAGTCGAGA TGCTATTTGT GCTTCAATAA AGGATATGTT TGAGGAGAAA AGAAGTATCC 480

TTGAACCTGC TGGTGCCCTT GCATTGGCTG GGGCTGAAGC CTACTGCAAA TACTATAACT 540

TGAAAGGAGA AACTGTGGTT GCAATAACTA GTGGGGCAAA TATGAACTTT GATCGACTTA 600

GACTAGTAAC CGAGCTAGCT GATGTTGGCC GAAAACGGGA AGCAGTGTTA GCTACATTTC 660

TGCCAGAGCG GCAGGGAAGC TTCAAAAAAT TCACAGAATT GGTTGGCAGG ATGAATATTA 720

CTGAATTCAA ATACAGATAC GATTCTAATG CAAAAGATGC CCTTGTTCTT TACAGTGTTG 780

GCATCTACAC TGACAATGAG CTTGGAGCAA TGATGGATCG CATGGAATCT GCGAAACTGA 840

GGACTGTTAA CCTTACTGAC AATGATTTGG CAAAGGACCA CCTTAGATAC TTTATTGGAG 900

GAAGATCAGA AATAAAAGAT GAACTGGTTT ACCGGTTCAT TTTCCCGGAA AGGCCTGGGG 960

CCCTTATGAA ATTTTTGGAC ACGTTTAGTC CTCGTTGGAA CATCAGCCTT TTCCATTACC 1020

GTGCACAGGG TGAAGCTGGA GCAAATGTAT TAGTTGGTAT ACAAGTGCCG CCAGCAGAAT 1080

TTGATGAATT CAAGAGTCAT GCCAACAATC TTGGGTACGA GTACATGTCA GAGCACAACA 1140

ATGAGATATA CCGGTTGCTG TTGCGTGACC CAAAGGTCTA ATGTATATGC CTTTGCTCCC 1200

ATAATAAGTT GGTGACACTT TTCAAGGAAG ATTTTGCTCC AAGGTAGAAG TTGCGAGTTT 1260

CTTCAAGTTG AAATGAAGCC ATCACCAAAT GTAGCTTCGG TGTGCCATCT GTTTACTCAG 1320

TTAGATCATG TAGTGTATCA GTTGTGTATC TTTGTTGTTG TGCTTCGTGA TCTCAATTTA 1380

TTGCTTTGTG CACCTAGAGG TTGTCAAATA ATGATAACCG ATATGTTATC TAAATATCTA 1440

ATAATGATTA TGTGATTGTG ATTAAAAAGG GGGGGCCC 1478

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: cen1.pk0064.f4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
Thr Val Val Leu Glu Gly Asp Ser Tyr Asp Glu Ala Gln Ser Tyr Ala
1               5                   10                  15

Lys Leu Arg Cys Gln Gln Glu Gly Arg Thr Phe Val Pro Pro Phe Asp
            20                  25                  30

His Pro Asp Val Ile Thr Gly Gln Gly Thr Ile Gly Met Glu Ile Val
        35                  40                  45

Arg Gln Leu Gln Gly Pro Leu His Ala Ile Phe Val Pro Val Gly Gly
    50                  55                  60

Gly Gly Leu Ile Ala Gly Ile Ala Ala Tyr Val Lys Arg Val Arg Pro
65                  70                  75                  80

Glu Val Lys Ile Ile Gly Val Glu Pro Ser Asp Ala Asn Ala Met Ala
                85                  90                  95

Leu Ser Leu Cys His Gly Lys Arg Val Met Leu Glu His Val Gly Gly
            100                 105                 110

Phe Ala Asp Gly Val Ala Val Lys Ala Val Gly Glu Glu Thr Phe Arg
        115                 120                 125

Leu Cys Arg Glu Leu Val Asp Gly Ile Val Met Val Ser Arg Asp Ala
    130                 135                 140

Ile Cys Ala Ser Ile Lys Asp Met Phe Glu Glu Lys Arg Ser Ile Leu
145                 150                 155                 160

Glu Pro Ala Gly Ala Leu Ala Leu Ala Gly Ala Glu Ala Tyr Cys Lys
                165                 170                 175

Tyr Tyr Asn Leu Lys Gly Glu Thr Val Val Ala Ile Thr Ser Gly Ala
            180                 185                 190

Asn Met Asn Phe Asp Arg Leu Arg Leu Val Thr Glu Leu Ala Asp Val
        195                 200                 205

Gly Arg Lys Arg Glu Ala Val Leu Ala Thr Phe Leu Pro Glu Arg Gln
    210                 215                 220
```

Gly Ser Phe Lys Lys Phe Thr Glu Leu Val Gly Arg Met Asn Ile Thr
225 230 235 240

Glu Phe Lys Tyr Arg Tyr Asp Ser Asn Ala Lys Asp Ala Leu Val Leu
245 250 255

Tyr Ser Val Gly Ile Tyr Thr Asp Asn Glu Leu Gly Ala Met Met Asp
260 265 270

Arg Met Glu Ser Ala Lys Leu Arg Thr Val Asn Leu Thr Asp Asn Asp
275 280 285

Leu Ala Lys Asp His Leu Arg Tyr Phe Ile Gly Gly Arg Ser Glu Ile
290 295 300

Lys Asp Glu Leu Val Tyr Arg Phe Ile Phe Pro Glu Arg Pro Gly Ala
305 310 315 320

Leu Met Lys Phe Leu Asp Thr Phe Ser Pro Arg Trp Asn Ile Ser Leu
325 330 335

Phe His Tyr Arg Ala Gln Gly Glu Ala Gly Ala Asn Val Leu Val Gly
340 345 350

Ile Gln Val Pro Pro Ala Glu Phe Asp Glu Phe Lys Ser His Ala Asn
355 360 365

Asn Leu Gly Tyr Glu Tyr Met Ser Glu His Asn Asn Glu Ile Tyr Arg
370 375 380

Leu Leu Leu Arg Asp Pro Lys Val
385 390

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 728 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: sfl1.pk0055.h7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAATATTGT AGCAATAACC AGTGGAGCAA ACATGAATTT TGATAAACTT CGGGTTGTAA 60

CTGAACTTGC TAATGTTGGT CGTAAACAAG AGGCTGTGCT GGCAACTGTT ATGGCAGAGG 120

AGCCTGGCAG TTTCAAACAA TTTTGTGAAT TGGTGGGGCA GATGAACATA ACAGAATTCA 180

AATACAGATA TAACTCAAAT GAGAAGGCAG TTGTCCTTTA CAGTGTTGGG GTTCACACAA 240

TCTCCGAACT AAGAGCAATG CAGGAGAGGA TGGAATCTTC TCAGCTCAAA ACTTACAATC 300

TCACAGAAAG TGACTTGGTG AAAGACCACT TGCGTTACTT GATGGGAGGC CGATCAAACG 360

TTCAGAATGA GGTCTTTGTC GTCTCACCTT TCCAAGAAAG ACTGGTGCTT TGATGAAATT 420

TTTGGACCCT TCAGTCCACG TTGGGATATT AGTTTATCCA TTACCGAGGG GAGGTGAAAC 480

TGGAGCAAAC TGCTAGTTGG NTACAGGTAC CAAAATGAGA TAGATGAGTC CATGATCGTG 540

CTAACAAACT GGATATGATT ATAAGTGGNA ATATGTGATG NCTCAGCTCA ATCNCGATGG 600

GGNTTAAGCA CTGCATATGG GNATTAGGGG NAGNTACANT TAAATTCACG GCCTCAAGNT 660

AAGCATANTN TAGGAACTAG CTTTACAGGG GGCTACNANT TAACCGNGTA TTTTTTTTGA 720

GATGANNG 728

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: sfl1.pk0055.h7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Asn Ile Val Ala Ile Thr Ser Gly Ala Asn Met Asn Phe Asp Lys Leu
1 5 10 15

Arg Val Val Thr Glu Leu Ala Asn Val Gly Arg Lys Gln Glu Ala Val
20 25 30

Leu Ala Thr Val Met Ala Glu Glu Pro Gly Ser Phe Lys Gln Phe Cys
35 40 45

Glu Leu Val Gly Gln Met Asn Ile Thr Glu Phe Lys Tyr Arg Tyr Asn
50 55 60

Ser Asn Glu Lys Ala Val Val Leu Tyr Ser Val Gly Val His Thr Ile
65 70 75 80

Ser Glu Leu Arg Ala Met Gln Glu Arg Met Glu Ser Ser Gln Leu Lys
85 90 95

Thr Tyr Asn Leu Thr Glu Ser Asp Leu Val Lys Asp His Leu Arg Tyr
100 105 110

Leu Met Gly Gly Arg Ser Asn Val Gln Asn Glu Val Phe Val Val Ser
115 120 125

Pro Xaa Pro Arg Lys Thr Gly Ala Leu Met Lys Phe Leu Asp Xaa Phe
130 135 140

Ser Pro Arg Trp Asp Ile Ser Leu
145 150

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 572 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: sre.pk0044.f3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
AAAGACCTGG TGCTTTGATG AAATTTTTGG ACCCCTTCAG TCCACGTTGG AATATCAGTT      60
TATTCCATTA CCGAGGGGAG GGTGAAACTG GAGCAAATGT GCTAGTTGGA ATACAGGTAC     120
CCAAAAGTGA GATGGATGAG TTCCACGATC GTGCCAACAA ACTTGGATAT GATTATAAAG     180
TGGTGAATAA TGATGATGAC TTCCAGCTTC TAATGCACTG ATGATGGTTT TAGGCACTTG     240
CCATTATTGT GTATTTTAGT CAACAAGTTT GCCATATTTA ATATTTCCAC GGTCGTTTCT     300
AAAAGTTGGA TGGGGAAAAA AGGTGGAAAG GAAGTGGCCT TCAGACATGT CATTAGTTGA     360
TTAGAGGAAC AACTAGTTCT TTTTACCTAA TGCGGCGTCT TATTACATTT TTTATAATCT     420
GTAATTTATG TTTTTTTGTT GTTGTTAACA TTGGAATCTT ATAATGTTGT TGCCTGGTCT     480
TTTGTGTCTG TAATATAAGT GTCTTCAAAA GGTTGTTTGC TAAATTTCAG CAGCCTAAAA     540
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                                   572
```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: sre.pk0044.f3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
Arg Pro Gly Ala Leu Met Lys Phe Leu Asp Pro Phe Ser Pro Arg Trp
1               5                   10                  15

Asn Ile Ser Leu Phe His Tyr Arg Gly Glu Gly Glu Thr Gly Ala Asn
            20                  25                  30

Val Leu Val Gly Ile Gln Val Pro Lys Ser Glu Met Asp Glu Phe His
        35                  40                  45

Asp Arg Ala Asn Lys Leu Gly Tyr Asp Tyr Lys Val Val Asn Asn Asp
    50                  55                  60

Asp Asp Phe Gln Leu Leu Met His
65                  70
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 507 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Burkholderia capacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Ser His Asp Tyr Leu Lys Lys Ile Leu Thr Ala Arg Val Tyr
1 5 10 15

Asp Val Ala Phe Glu Thr Glu Leu Glu Pro Ala Arg Asn Leu Ser Ala
20 25 30

Arg Leu Arg Asn Pro Val Tyr Leu Lys Arg Glu Asp Asn Gln Pro Val
35 40 45

Phe Ser Phe Lys Leu Arg Gly Ala Tyr Asn Lys Met Ala His Ile Pro
50 55 60

Ala Asp Ala Leu Ala Arg Gly Val Ile Thr Ala Ser Ala Gly Asn His
65 70 75 80

Ala Gln Gly Val Ala Phe Ser Ala Ala Arg Met Gly Val Lys Ala Val
85 90 95

Ile Val Val Pro Val Thr Thr Pro Gln Val Lys Val Asp Ala Val Arg
100 105 110

Ala His Gly Gly Pro Gly Val Glu Val Ile Gln Ala Gly Glu Ser Tyr
115 120 125

Ser Asp Ala Tyr Ala His Ala Leu Lys Val Gln Glu Glu Arg Gly Leu
130 135 140

Thr Phe Val His Pro Phe Asp Asp Pro Tyr Val Ile Ala Gly Gln Gly
145 150 155 160

Thr Ile Ala Met Glu Ile Leu Arg Gln His Gln Gly Pro Ile His Ala
165 170 175

Ile Phe Val Pro Ile Gly Gly Gly Gly Leu Ala Ala Gly Val Ala Ala
180 185 190

Tyr Val Lys Ala Val Arg Pro Glu Ile Lys Val Ile Gly Val Gln Ala
195 200 205

Glu Asp Ser Cys Ala Met Ala Gln Ser Leu Gln Ala Gly Lys Arg Val
210 215 220

Glu Leu Ala Glu Val Gly Leu Phe Ala Asp Gly Thr Ala Val Lys Leu
225 230 235 240

Val Gly Glu Glu Thr Phe Arg Leu Cys Lys Glu Tyr Leu Asp Gly Val
245 250 255

Val Thr Val Asp Thr Asp Ala Leu Cys Ala Ala Ile Lys Asp Val Phe
260 265 270

Gln Asp Thr Arg Ser Val Leu Glu Pro Ser Gly Ala Leu Ala Val Ala
275 280 285

Gly Ala Lys Leu Tyr Ala Glu Arg Glu Gly Ile Glu Asn Gln Thr Leu
290 295 300

Val Ala Val Thr Ser Gly Ala Asn Met Asn Phe Asp Arg Met Arg Phe
305 310 315 320

Val Ala Glu Arg Ala Glu Val Gly Glu Ala Arg Glu Ala Val Phe Ala
325 330 335

Val Thr Ile Pro Glu Glu Arg Gly Ser Phe Lys Arg Phe Cys Ser Leu
340 345 350

Val Gly Asp Arg Asn Val Thr Glu Phe Asn Tyr Arg Ile Ala Asp Ala
355 360 365

Gln Ser Ala His Ile Phe Val Gly Val Gln Ile Arg Arg Arg Gly Glu
370 375 380

Ser Ala Asp Ile Ala Ala Asn Phe Glu Ser His Gly Phe Lys Thr Ala
385 390 395 400

Asp Leu Thr His Asp Glu Leu Ser Lys Glu His Ile Arg Tyr Met Val
405 410 415

Gly Gly Arg Ser Pro Leu Ala Leu Asp Glu Arg Leu Phe Arg Phe Glu
420 425 430

Phe Pro Glu Arg Pro Gly Ala Leu Met Lys Phe Leu Ser Ser Met Ala
435 440 445

Pro Asp Trp Asn Ile Ser Leu Phe His Tyr Arg Asn Gln Gly Ala Asp
450 455 460

Tyr Ser Ser Ile Leu Val Gly Leu Gln Val Pro Gln Ala Asp His Ala
465 470 475 480

Glu Phe Glu Arg Phe Leu Ala Ala Leu Gly Tyr Pro Tyr Val Glu Glu
485 490 495

Ser Ala Asn Pro Ala Tyr Arg Leu Phe Leu Ser
500 505

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: cc3.mn0002d2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACGAGACGAG TCCCCTCCCC CCACCTCGCC TCACCCAACC GGAACGAACA AGTTACCATC 60

TCATCCCAAC CCCGCCTCGA CCGGATCTCG TCGGACTCGG ATCCGCCCGA CCACCCCGCG 120

CCGCCGCAGA TCAAAGAAGA TGGCAGCTCT CGACACCTTC CTCTTCACCT CGGAGTCTGT 180

GAACGAGGGA CACCCTGACA AGCTCTGCGA CCAGGTCTCA GATGCCGTTC TTGACGCTTG 240

CCTTGCTGAG GACCCTGACA GCAAGGTTGC TTGTGAGACC TGCACCAAGA CCAACATGGT 300

CATGGTCTTT GGTGAGATCA CCACCAAGGC CAATGTCGAC TACGAGAAGA TTGTCAGGGA 360

GACCTGCCGC AACATTGGTT TTGTGTCAAA CGATGTCGGG CTTGACGCTG ACCACTGCAA 420

GGTGCTCGTG AACATTGAGC AGCAGTCCCC TGATATTGCT CAGGGTGTGC ATGGCCACTT 480

CACCAAGCGC CCCGAGGAGA TTGGAGCTGG TGACCAGGGA CACATGTTCG GGTATGCGAC 540

CGATGAGACC CCTGAGTTGA TGCCCCTCAG CCATGTCCTT GCCACCAAGC TAGGTGCTCG 600
TCTCACCGAG GTCCGCAAGA ACGGAACCTG CCCCTGGCTC AGGCCTGATG GGAAGACCCA 660
GGTGACAGTC GAGTACCGCA ATGAGGGTGG TGCCATGGTC CCCATCCGTG TCCACACCGT 720
CCTCATCTCC ACCCAGCACG ACGAGACAGT GACCAATGAT GAGATCGCTG CTGACCTGAA 780
GGAGCATGTC ATCAAGCCTA TCATCCCTGA GCAGTACCTT GACGAGAAGA CCATCTTCCA 840
CCTTAACCCA TCCGGCCGCT TTGTCATTGG TGGACCTCAC GGCGATGCTG GCCTCACTGG 900
CCGCAAGATC ATCATTGACA CCTACGGTGG CTGGGGAGCC CATGGCGGTG GCGCTTTCTC 960
CGGCAAGGAC CCAACCAAGG TTGACCGCAG CGGAGCCTAT GTCGCGAGGC AGGCTGCCAA 1020
GAGCATCGTC GCCAGCGGCC TTGCTCGCCG CGCCATCGTC CAGGTGTCCT ACGCCATCGG 1080
CGTGCCCGAG CCTCTCTCCG TGTTTGTCGA CACGTACGGC ACCGGCGCGA TCCCCGACAA 1140
GGAGATCCTC AAGATTGTCA AGGAGAACTT CGATTTCAGG CCTGGCATGA TTATCATCAA 1200
CCTTGACCTC AAGAAAGGCG GCAACGGGCG CTACCTCAAG ACGGCAGCCT ACGGCCACTT 1260
CGGAAGGGAC GACCCTGACT TCACCTGGGA GGTGGTGAAG CCACTCAAGT CGGAGAAACC 1320
TTCTGCCTAA GGCGGCCTTT TTTTCAGTAA GAAGCTTTTG GTGGTCTGCT GTGCTTAATC 1380
ATGCTTTTAT ATGGCTTCTA CATGTTGTGG TTCTTTCTTG ATCTGCACCG CGCTTATCGT 1440
TTGTGTTGTA CTGCCCTAAT AAGTGGTGCT TATGAGGACT GTTTCTGGTT TTGCTGCTTA 1500
TGTTGTAATG CTTTGAAACA ATGAAAGAAG CTACAGGCCA CAGCTATTTT GAGAAGTAAT 1560
GGAACCTCGT GCCGTTTTGA TT 1582

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: cc3.mn0002.d2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Ala Leu Asp Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu
1 5 10 15

Gly His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp
20 25 30

Ala Cys Leu Ala Glu Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys
35 40 45

Thr Lys Thr Asn Met Val Met Val Phe Gly Glu Ile Thr Thr Lys Ala
50 55 60

Asn Val Asp Tyr Glu Lys Ile Val Arg Glu Thr Cys Arg Asn Ile Gly
65 70 75 80

Phe Val Ser Asn Asp Val Gly Leu Asp Ala Asp His Cys Lys Val Leu
85 90 95

Val Asn Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly
100 105 110

His Phe Thr Lys Arg Pro Glu Glu Ile Gly Ala Gly Asp Gln Gly His
115 120 125

Met Phe Gly Tyr Ala Thr Asp Glu Thr Pro Glu Leu Met Pro Leu Ser
130 135 140

His Val Leu Ala Thr Lys Leu Gly Ala Arg Leu Thr Glu Val Arg Lys
145 150 155 160

Asn Gly Thr Cys Pro Trp Leu Arg Pro Asp Gly Lys Thr Gln Val Thr
165 170 175

Val Glu Tyr Arg Asn Glu Gly Gly Ala Met Val Pro Ile Arg Val His
180 185 190

Thr Val Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu
195 200 205

Ile Ala Ala Asp Leu Lys Glu His Val Ile Lys Pro Ile Ile Pro Glu
210 215 220

Gln Tyr Leu Asp Glu Lys Thr Ile Phe His Leu Asn Pro Ser Gly Arg
225 230 235 240

Phe Val Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys
245 250 255

Ile Ile Ile Asp Thr Tyr Gly Gly Trp Gly Ala His Gly Gly Gly Ala
260 265 270

Phe Ser Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Val
275 280 285

Ala Arg Gln Ala Ala Lys Ser Ile Val Ala Ser Gly Leu Ala Arg Arg
290 295 300

Ala Ile Val Gln Val Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser
305 310 315 320

Val Phe Val Asp Thr Tyr Gly Thr Gly Ala Ile Pro Asp Lys Glu Ile
325 330 335

Leu Lys Ile Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ile
340 345 350

Ile Asn Leu Asp Leu Lys Lys Gly Gly Asn Gly Arg Tyr Leu Lys Thr
355 360 365

Ala Ala Tyr Gly His Phe Gly Arg Asp Asp Pro Asp Phe Thr Trp Glu
370 375 380

Val Val Lys Pro Leu Lys Ser Glu Lys Pro Ser Ala
385 390 395

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2183 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Oryza sativa

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
GAATTCTTAT AAATGAACGG AAAATGGAAA AAAAAATTGA TTGGTGCCAC TTCAAAGTTA     60
AATATGCCAA GACGAATTGA TATGTTTCTG CTGTTGTTTT ATGCTCTTGA TTAGTTGATG    120
CGCATGTTCA ATGATTTATG ATGTTTGTCT TTGTGGAAAG ATTACATGTA AAGAGTATAG    180
TAGAACCCCT AAAAGCTAGC CAGCGATTTC GCTCTTTTTT TCCAGGTCTC CATGATATGT    240
TTACCCCTAA AAGTGGTATA TTTATGTGAT AGTTACAATA CATAGTGGAC CACGATTGAT    300
TATGCGTTTA TGCTGATTCC GGCAGAAAAT TGTTAGATTC CTTGTGCTCT ATACCTGCTT    360
GTTGCGCTTG TAGAGAATAT TACAAATACC TAACACTTGC CCAAGGAACT TAGGAACTTA    420
GTCAACTCTT TGTAGGGACA ACTATTTTAG CCCAAAATTG TGGTCTTGTC AGGTGCCAAC    480
AAAACAGCAT CTTGGCGTAC ATAAGCTATA TAGAGGATTA AAAGGAATGT TTTGTTCCTT    540
GCTACTGTTT TTTTAACCTG TTTACTCAGG ACAAATTTTG TTGCATAAAC CATTTGTTCT    600
AGGGATCAGT ATTGTCCTCT CAGTGTGTTA TGTAAGCATT TCCAGAAATC AATTGTCGCT    660
ATCAGCTTCC CTCACATTAG CTATCACTTA TACCCCTTTT TTTCTCATAG GCTCACCATG    720
TCCATTTTAT TCATGATATT TCTTTGTCTA AAGTATGTGA AATACCATTT TATGCAGATA    780
GGAGAAGATG GCCGCACTTG ATACCTTCCT CTTTACCTCG GAGTCTGTGA ACGAGGGCCA    840
CCCTGACAAG CTCTGCGACC AAGTCTCAGA TGCTGTGCTT GATGCCTGCC TCGCCGAGGA    900
CCCTGACAGC AAGGTCGCTT GTGAGACCTG CACCAAGACA AACATGGTCA TGGTCTTTGG    960
TGAGATCACC ACCAAGGCTA ACGTTGACTA TGAGAAGATT GTCAGGGAGA CATGCCGTAA   1020
CATCGGTTTT GTGTCAGCTG ATGTCGGTCT CGATGCTGAC CACTGCAAGG TGCTTGTGAA   1080
CATCGAGCAG CAGTCCCCTG ACATTGCACA GGGTGTGCAC GGGCACTTCA CCAAGCGCCC   1140
TGAGGAGATT GGTGCTGGTG ACCAGGGACA CATGTTTGGA TATGCAACTG ATGAGACCCC   1200
TGAGTTGATG CCCCTCAGCC ATGTCCTTGC TACCAAGCTT GGCGCTCGTC TTACGGAGGT   1260
TCGCAAGAAT GGGACCTGCG CATGGCTCAG GCCTGACGGG AAGACCCAAG TGACTGTTGA   1320
GTACCGCAAT GAGAGCGGTG CCAGGGTCCC TGTCCGTGTC CACACCGTCC TCATCTCTAC   1380
CCAGCATGAT GAGACAGTCA CCAACGATGA GATTGCTGCT GACCTGAAGG AGCATGTCAT   1440
CAAGCCTGTC ATTCCCGAGC AGTACCTTGA TGAGAAGACA ATCTTCCATC TTAACCCATC   1500
TGGTCGCTTC GTCATTGGCG GACCTCATGG TGATGCTGGT CTCACTGGCC GGAAGATCAT   1560
CATTGACACT TATGGTGGCT GGGGAGCTCA CGGTGGTGGT GCCTTCTCTG GCAAGGACCC   1620
AACCAAGGTT GACCGCAGTG GAGCATACGT CGCAAGGCAA GCTGCCAAGA GCATTGTTGC   1680
```

TAGTGGCCTT GCTCGCCGCT GCATTGTCCA AGTATCATAC GCCATCGGTG TCCCAGAGCC 1740

ACTGTCCGTA TTCGTCGACA CATACGGCAC TGGCAGGATC CCTGACAAGG AGATCCTCAA 1800

GATTGTGAAG GAGAACTTCG ACTTCAGGCC TGGCATGATC ATCATCAACC TTGACCTCAA 1860

GAAAGGCGGC AACGGACGCT ACCTCAAGAC GGCGGCTTAC GGTCACTTCG GAAGGGACGA 1920

CCCAGACTTC ACCTGGGAGG TGGTGAAGCC CCTCAAGTGG GAGAAGCCTT CTGCCTAAAA 1980

GCTCCCTTTC GGAGGCTTTT GCTCTGTCCC ATTATGGTGT TTTGTTTCCT CGCTGCTCAG 2040

CATTGTGATT CTTAACCTGC CCCCCGCTGC CATTTATGCC CATGCACGCT ACTTTCCTAA 2100

TAATAAGTAC TTATAAGGGT ATTGTGTTTG AATATTTTAC CTAGAGGAGG AGGAGGATTT 2160

GTTATCTGTT ATTGCTTAAG CTT 2183

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: s2.12b06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGCCAAGCCC CACTCAACCA CCACACCACT CTCTCTGCTC TTCTTCTACC TTTCAAGTTT 60

TTAAAGTATT AAGATGGCAG AGACATTCCT ATTTACCTCA GAGTCAGTGA ACGAGGGACA 120

CCCTGACAAG CTCTGCGACC AAATCTCCGA TGCTGTCCTC GACGCTTGCC TTGAACAGGA 180

CCCAGACAGC AAGGTTGCCT GCGAAACATG CACCAAGACC AACTTGGTCA TGGTCTTCGG 240

AGAGATCACC ACCAAGGCCA ACGTTGACTA CGAGAAGATC GTGCGTGACA CCTGCAGGAA 300

CATCGGCTTC GTCTCAAACG ATGTGGGACT TGATGCTGAC AACTGCAAGG TCCTTGTAAA 360

CATTGAGCAG CAGAGCCCTG ATATTGCCCA GGGTGTGCAC GGCCACCTTA CCAAAAGACC 420

CGAGGAAATC GGTGCTGGAG ACCAGGGTCA CATGTTTGGC TATGCCACGG ACGAAACCCC 480

AGAATTGATG CCATTGAGTC ATGTTCTTGC AACTAAACTC GGTGCTCGTC TCACCGAGGT 540

TCGCAAGAAC GGAACCTGCC CATGGTTGAG GCCTGATGGG AAAACCCAAG TGACTGTTGA 600

GTATTACAAT GACAACGGTG CCATGGTTCC AGTTCGTGTC CACACTGTGC TTATCTCCAC 660

CCAACATGAT GAGACTGTGA CCAACGACGA AATTGCAGCT GACCTCAAGG AGCATGTGAT 720

CAAGCCGGTG ATCCCGGAGA AGTACCTTGA TGAGAAGACC ATTTTCCACT TGAACCCCTC 780

TGGCCGTTTT GTCATTGGAG GTCCTCACGG TGATGCTGGT CTCACCGGCC GCAAGATCAT 840

CATCGATACT TACGGAGGAT GGGGTGCTCA TGGTGGTGGT GCTTTCTCCG GGAAGGATCC 900

CACCAAGGTT GATAGGAGTG GTGCTTACAT TGTGAGACAG GCTGCTAAGA GCATTGTGGC 960

AAGTGGACTA GCCAGAAGGT GCATTGTGCA AGTGTCTTAT GCCATTGGTG TGCCCGAGCC 1020

TTTGTCTGTC TTTGTTGACA CCTATGGCAC CGGGAAGATC CATGATAAGG AGATTCTCAA 1080

CATTGTGAAG GAGAACTTTG ATTTCAGGCC CGGTATGATC TCCATCAACC TTGATCTCAA 1140

GAGGGGTGGG AATAACAGGT TCTTGAAGAC TGCTGCATAT GGACACTTCG GCAGAGAGGA 1200

CCCTGACTTC ACATGGGAAG TGGTCAAGCC CCTCAAGTGG GAGAAGGCCT AAGGCCATTC 1260

ATTCCACTGC AATGTGCTGG GAGTTTTTTA GCGTTGCCCT TATAATGTCT ATTATCCATA 1320

ACTTTCCACG TCCCTTGCTC TGTGTTTTTC TCTCGTCGTC CTCCTCCTAT TTTGTTTCTC 1380

CTGCCTTTCA TTTGTAATTT TTTACATGAT CAACTAAAAA ATGTACTCTC TGTTTTCCGA 1440

CCATTGTGTC TCTTAATATC AGTATCAAAA AGAATGTTCC AAGTT 1485

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: s2.12b06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Ala Glu Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu Gly His
1 5 10 15

Pro Asp Lys Leu Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Cys
20 25 30

Leu Glu Gln Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys Thr Lys
35 40 45

Thr Asn Leu Val Met Val Phe Gly Glu Ile Thr Thr Lys Ala Asn Val
50 55 60

Asp Tyr Glu Lys Ile Val Arg Asp Thr Cys Arg Asn Ile Gly Phe Val
65 70 75 80

Ser Asn Asp Val Gly Leu Asp Ala Asp Asn Cys Lys Val Leu Val Asn
85 90 95

Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly His Leu
100 105 110

Thr Lys Arg Pro Glu Glu Ile Gly Ala Gly Asp Gln Gly His Met Phe
115 120 125

Gly Tyr Ala Thr Asp Glu Thr Pro Glu Leu Met Pro Leu Ser His Val
130 135 140

Leu Ala Thr Lys Leu Gly Ala Arg Leu Thr Glu Val Arg Lys Asn Gly
145 150 155 160

Thr Cys Pro Trp Leu Arg Pro Asp Gly Lys Thr Gln Val Thr Val Glu
165 170 175

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Tyr Tyr Asn Asp Asn Gly Ala Met Val Pro Val Arg Val His Thr Val
            180                 185                 190

Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu Ile Ala
        195                 200                 205

Ala Asp Leu Lys Glu His Val Ile Lys Pro Val Ile Pro Glu Lys Tyr
    210                 215                 220

Leu Asp Glu Lys Thr Ile Phe His Leu Asn Pro Ser Gly Arg Phe Val
225                 230                 235                 240

Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile
                245                 250                 255

Ile Asp Thr Tyr Gly Gly Trp Gly Ala His Gly Gly Gly Ala Phe Ser
            260                 265                 270

Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Ile Val Arg
        275                 280                 285

Gln Ala Ala Lys Ser Ile Val Ala Ser Gly Leu Ala Arg Arg Cys Ile
    290                 295                 300

Val Gln Val Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser Val Phe
305                 310                 315                 320

Val Asp Thr Tyr Gly Thr Gly Lys Ile His Asp Lys Glu Ile Leu Asn
                325                 330                 335

Ile Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ser Ile Asn
            340                 345                 350

Leu Asp Leu Lys Arg Gly Gly Asn Asn Arg Phe Leu Lys Thr Ala Ala
        355                 360                 365

Tyr Gly His Phe Gly Arg Glu Asp Pro Asp Phe Thr Trp Glu Val Val
    370                 375                 380

Lys Pro Leu Lys Trp Glu Lys Ala
385                 390
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1479 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

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GAATTCCTAC AAAGAGGTTA TTTCTCTCAA GGGGTAAAAA GATTGCCCCT TTTCGACATT    60

TATAATCCTC TTTTTCTCTT TGTTCGCCGT TGGGTTCTTC ACTTTCCTGT TTCTTGAGAA   120

TGGAAACTTT CTTATTCACC TCCGAGTCTG TGAACGAGGG TCACCCAGAC AAGCTCTGTG   180

ATCAGATCTC TGATGCAGTT CTTGATGCCT GCCTTGAGCA AGATCCCGAG AGCAAAGTTG   240

CATGTGAAAC TTGCACCAAG ACCAACTTGG TCATGGTCTT TGGTGAGATC ACAACCAAGG   300
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CTATTGTAGA CTATGAGAAG ATTGTGCGTG ACACATGCCG TAATATTGGA TTTGTTTCTG 360

ATGATGTTGG TCTTGATGCT GACAACTGCA AGGTCCTTGT TTACATTGAG CAGCAAAGTC 420

CTGATATTGC TCAAGGTGTC CACGGCCATC TGACCAAACG CCCCGAGGAG ATTGGTGCTG 480

GTGACCAGGG CCACATGTTT GGCTATGCAA CAGATGAGAC CCCTGAATTA ATGCCTCTCA 540

GTCACGTGCT TGCAACTAAA CTTGGTGCCC GTCTTACAGA AGTCCGCAAG AATGGCACCT 600

GCGCCTGGTT GAGGCCTGAT GGCAAGACCC AAGTTACTGT TGAGTATAGC AATGACAATG 660

GTGCCATGGT TCCAATTAGG GTACACACTG TTCTTATCTC CACCCAACAC GATGAGACCG 720

TTACCAATGA TGAGATTGCC CGCGACCTTA AGGAGCATGT CATCAAACCA GTCATCCCAG 780

AGAAGTACCT TGATGAGAAT ACTATTTTCC ACCTTAACCC ATCTGGCCGA TTCGTTATTG 840

GTGGACCTCA TGGTGATGCT GGTCTCACTG GTCGTAAAAT CATCATCGAC ACTTATGGTG 900

GTTGGGGTGC TCATGGTGGT GGTGCTTTCT CGGGCAAAGA CCCAACCAAG GTCGACAGGA 960

GTGGTGCATA CATTGTAAGG CAGGCTGCAA AGAGTATCGT AGCTAGTGGA CTTGCTCGTA 1020

GATGCATCGT GCAGGTATCT TATGCCATCG GTGTGCCTGA GCCATTGTCT GTATTCGTTG 1080

ACACCTATGG CACTGGAAAG ATCCCTGACA GGGAAATTTT GAAGATCGTT AAGGAGAACT 1140

TTGACTTCAG ACCTGGAATG ATGTCCATTA ACTTGGATTT GAAGAGGGGT GGCAATAGAA 1200

GATTCTTGAA AACTGCTGCC TATGGTCACT TTGGACGTGA TGACCCCGAT TTCACATGGG 1260

AAGTTGTCAA GCCCCTCAAG TGGGAAAAGC CCCAAGACTA ATAAGTGCTT GCCTATGTTT 1320

TTGTTCTTTG TTGTTTGCTT GTGGCTTTAG AATCTCCCCC GTGTTTGCTT GTTTGTCTTT 1380

GTATTTTCTC TTTTGACCCT TTATTTTGTT ATTGTCCTGT TTCCATTGTG TTGGATGGAT 1440

ATCTTAGGCC TTGGAATATT AAGGAAAGAA AAGGAATTC 1479

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCTCCCTTC GGTTCATCGG CCTCCCGATC GAGCAGTAGA AGCAGCGCAA GGGCATCGCT 60

AGCACTAAAG AAATGGCAGC CGAGACGTTC CTCTTCACGT CCGAGTCTGT GAACGAGGGC 120

CATCCCGACA AGCTCTGTGA CCAAGTCTCC GACGCCGTCT TGGATGCCTG CTTGGCCCAG 180

GATGCCGACA GCAAGGTCGC CTGCGAGACC GTCACCAAGA CCAACATGGT CATGGTCTTG 240

GGCGAGATCA CCACCAAGGC CACCGTCGAC TATGAGAAGA TCGTGCGTGA CACCTGCCGC 300

AACATCGGTT TCATCTCTGA TGACGTTGGT CTCGACGCCG ACCGTTGCAA RGTGCTCGTC 360

AACATCGAGC AGCAGTCCCC TGACATTGCC CAGGGTGTTC ATGGACACTT CACCAAGCGT 420

CCCGAAGAAG TCGGCGCCGG TGACCAGGGC ATCATGTTCG GCTATGCCAC CGATGAGACC 480

CCTGAGCTGA TGCCCCTCAA GCACGTGCTT GCCACCAAGC TYGGAGCTCG CCTCACSGAG 540

GTCCGCAAGA ATGGCACCTG CGCCTGGGTC AGGCCTGACG GAAAGACCCA GGTCACAGTC 600

GAGTACCTAA ACGAGGATGG TGCCATGGTA CCTGTTCGTG TGCACACCGT CCTCATCTCC 660

ACCCAGCACG ACGAGACCGT CACCAACGAC GAGATTGCTG CGGACCTCAA GGAGCATGTC 720

ATCAAGCCGG TGATCCCCGC AAAGTACCTC GATGAGAACA CCATCTTCCA CCTGAACCCG 780

TCTGGCCGCT TCGTCATCGG CGGCCCCCAC GGTGACGCCG GTCTCACCGG CCGCAAGATC 840

ATCATCGACA CCTATGGTGG CTGGGGAGCC CACGGCGGCG GTGCCTTCTC TGGCAAGGAC 900

CCAACCAAGG TCGACCGYAG TGGCGCCTAC ATTGCCAGGC ARGCCGCCAA GAGCATCATC 960

GCCAGCGGCC TCGCACGCCG CTGCATTGTG CAGATCTCAT ACGCCATCGG TGTGCCTGAG 1020

CCTTTGTCTG TGTTCGTCGA CTCCTACGGC ACCGGCAAGA TCCCCGACAG GGAGATCCTC 1080

AAGCTCGTGA AGGAGAACTT TGACTTCAGG CCCGGGATGA TCAGCATCAA CCTGGACTTG 1140

AAGAAAGGTG GAAACAGGTT CATCAAGACC GCTGCTTACG GTCACTTTGG CCGTGATGAT 1200

GCCGACTTCA CCTGGGAGGT GGTGAAGCCC CTCAAGTTCG ACAAGGCATC TGCCTAAGAG 1260

CATGGCATTC TCTTGGTCTG CCGCCTCTCA AGTTCGTCAA GACGGGATCA TGTTGCTCCT 1320

GGGAAGTGGG AAGAAGCATT AGACATTGAA GCGACGCTCT ACACTGGTCT TGTTGTATGG 1380

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ala Ala Glu Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu Gly
1 5 10 15

His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp Ala
20 25 30

Cys Leu Ala Gln Asp Ala Asp Ser Lys Val Ala Cys Glu Thr Val Thr
35 40 45

Lys Thr Asn Met Val Met Val Leu Gly Glu Ile Thr Thr Lys Ala Thr
50 55 60

Val Asp Tyr Glu Lys Ile Val Arg Asp Thr Cys Arg Asn Ile Gly Phe
65 70 75 80

Ile Ser Asp Asp Val Gly Leu Asp Ala Asp Arg Cys Lys Val Leu Val
85 90 95

Asn Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly His
100 105 110

Phe Thr Lys Arg Pro Glu Glu Val Gly Ala Gly Asp Gln Gly Ile Met
115 120 125

Phe Gly Tyr Ala Thr Asp Glu Thr Pro Glu Leu Met Pro Leu Lys His
130 135 140

Val Leu Ala Thr Lys Leu Gly Ala Arg Leu Thr Glu Val Arg Lys Asn
145 150 155 160

Gly Thr Cys Ala Trp Val Arg Pro Asp Gly Lys Thr Gln Val Thr Val
165 170 175

Glu Tyr Leu Asn Glu Asp Gly Ala Met Val Pro Val Arg Val His Thr
180 185 190

Val Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu Ile
195 200 205

Ala Ala Asp Leu Lys Glu His Val Ile Lys Pro Val Ile Pro Ala Lys
210 215 220

Tyr Leu Asp Glu Asn Thr Ile Phe His Leu Asn Pro Ser Gly Arg Phe
225 230 235 240

Val Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile
245 250 255

Ile Ile Asp Thr Tyr Gly Gly Trp Gly Ala His Gly Gly Gly Ala Phe
260 265 270

Ser Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Ile Ala
275 280 285

Arg Gln Ala Ala Lys Ser Ile Ile Ala Ser Gly Leu Ala Arg Arg Cys
290 295 300

Ile Val Gln Ile Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser Val
305 310 315 320

Phe Val Asp Ser Tyr Gly Thr Gly Lys Ile Pro Asp Arg Glu Ile Leu
325 330 335

Lys Leu Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ser Ile
340 345 350

Asn Leu Asp Leu Lys Lys Gly Gly Asn Arg Phe Ile Lys Thr Ala Ala
355 360 365

Tyr Gly His Phe Gly Arg Asp Asp Ala Asp Phe Thr Trp Glu Val Val
370 375 380

Lys Pro Leu Lys Phe Asp Lys Ala Ser Ala
385 390

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Hordeum vulgare

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

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GAATTCCGGA TAGCATCAGC ACAACTGCAC GAGAGCATCT CTACCACCAA AGAAATGGCG     60
GCCGAGACGT TCCTCTTCAC GTCCGAGTCC GTGAACGAGG GCCATCCCGA CAAGCTGTGC    120
GACCAGGTCT CTGACGCCGT CTTGGACGCC TGCTTGGCCC AGGATCCTGA CAGCAAGGTT    180
GCTTGCGAGA CCTGCACCAA GACCAACATG GTCATGGTCT TCGGCGAGAT CACCACCAAG    240
GCCACCGTTG ACTATGAGAA GATTGTGCGC GACACCTGCC GTGACATCGG CTTCATCTCT    300
GACGACGTCG GTCTCGATGC CGACCATTGC AAGGTGCTCG TCAACATCGA GCAGCAATCC    360
CCTGACATTG CCCAGGGTGT TCACGGACAC TTCACCAAGC GTCCAGAAGA GGTCGGCGCC    420
GGTGACCAGG GCATCATGTT TGGCTACGCC ACTGATGAGA CCCCTGAGCT GATGCCCCTC    480
ACCCACATGC TTGCCACCAA GCTCGGAGCT CGCCTCACCG AGGTCCGCAA GAATGGCACC    540
TGCGCCTGGC TCAGGCCTGA TGGAAAGACC CAGGTCACCA TTGAGTACCT AAACGAGGGT    600
GGTGCCATGG TGCCCGTTCG TGTGCACACC GTCCTCATCT CCACCCAGCA TGATGAGACC    660
GTCACCAACG ATGAGATCGC TGCAGACCTC AAGGAGCATG TCATCAAGCC GGTGATTCCC    720
GGGAAGTACC TCGATGAGAA CACCATCTTC CACCTGAACC CATCGGGCCG CTTTGTCATC    780
GGTGGCCCTC ACGGCGATGC CGGTCTCACC GCCCGCAAGA TCATCATCGA CACCTATGGT    840
GGCTGGGGAG CCCACGGCGG CGGTGCCTTC TCTGGCAAGG ACCCTACCAA GGTCGACCGC    900
AGTGGCGCCT ACATTGCCAG GCAGGCTGCC AAGAGCATCA TCGCCAGCGG CCTCGCACGC    960
CGGTGCATTG TGCAGATCTC ATATGCCATC GGTGTACCTG AGCCTTTGTC TGTGTTCGTC   1020
GACTCCTACG GCACTGGCAA GATCCCTGAC AGGGAGATCC TCAAGCTCGT GAAGGAGAAC   1080
TTTGACTTCA GACCCGGGAT GATCACGATC AACCTCGACT TGAAGAAAGG TGGAAACAGG   1140
TTCATCAAGA CAGCTGCTTA CGGTCACTTT GGCCGCGATG ATGCTGACTT CACCTGGGAG   1200
GTGGTGAAGC CCCTCAAGTT CGACAAGGCA TCTGCTTAAG AAGAAGACAT CACATTGAGG   1260
GTTCTTCTTG GTCTGATGCC TCTCAAGTTC GGCAAGGCGG GATCCTTTTG CTCCTCGGAA   1320
GTAAGAAGAA GCATTCAACA TCGCCCGGAA TTC                                1353
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CLAIMS

What is claimed is:

1. An isolated nucleic acid fragment encoding all or a substantial portion of a plant dihydropicolinate reductase comprising a member selected from the group consisting of:

(a) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:2 and 4;

(b) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:2 and 4; and

(c) an isolated nucleic acid fragment that is complementary to (a) or (b).

2. The isolated nucleic acid fragment of Claim 1 wherein the nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in a member selected from the group consisting of SEQ ID NO:1 and 3.

3. A chimeric gene comprising the nucleic acid fragment of Claim 1 operably linked to suitable regulatory sequences.

4. A transformed host cell comprising the chimeric gene of Claim 3.

5. A dihydropicolinate reductase polypeptide comprising all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:2 and 4.

6. An isolated nucleic acid fragment encoding all or a substantial portion of a plant diaminopimelate epimerase comprising a member selected from the group consisting of:

(a) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:7, 9, 11, and 13;

(b) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:7, 9, 11, and 13; and

(c) an isolated nucleic acid fragment that is complementary to (a) or (b).

7. The isolated nucleic acid fragment of Claim 6 wherein the nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in a member selected from the group consisting of SEQ ID NO:6, 8, 10, and 12.

8. A chimeric gene comprising the nucleic acid fragment of Claim 6 operably linked to suitable regulatory sequences.

9. A transformed host cell comprising the chimeric gene of Claim 8.

10. A diaminopimelate epimerase polypeptide comprising all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO: 7, 9, 11, and 13.

11. An isolated nucleic acid fragment encoding all or a substantial portion of a plant threonine synthase comprising a member selected from the group consisting of:

(a) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:16 and 18;

(b) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:16 and 18; and

(c) an isolated nucleic acid fragment that is complementary to (a) or (b).

12. The isolated nucleic acid fragment of Claim 11 wherein the nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in a member selected from the group consisting of SEQ ID NO:15 and 17.

13. A chimeric gene comprising the nucleic acid fragment of Claim 11 operably linked to suitable regulatory sequences.

14. A transformed host cell comprising the chimeric gene of Claim 13.

15. A threonine synthase polypeptide comprising all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:16 and 18.

16. An isolated nucleic acid fragment encoding all or a substantial portion of a plant threonine synthase comprising a member selected from the group consisting of:

(a) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in SEQ ID NO:20;

(b) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in SEQ ID NO:20; and

(c) an isolated nucleic acid fragment that is complementary to (a) or (b).

17. The isolated nucleic acid fragment of Claim 16 wherein the nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in SEQ ID NO:19.

18. A chimeric gene comprising the nucleic acid fragment of Claim 16 operably linked to suitable regulatory sequences.

19. A transformed host cell comprising the chimeric gene of Claim 18.

20. A threonine synthase polypeptide comprising all or a substantial portion of the amino acid sequence set forth in SEQ ID NO:20.

21. An isolated nucleic acid fragment encoding all or a substantial portion of a plant threonine synthase comprising a member selected from the group consisting of:

(a) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:22 and 24;

(b) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:22 and 24; and

(c) an isolated nucleic acid fragment that is complementary to (a) or (b).

22. The isolated nucleic acid fragment of Claim 21 wherein the nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in a member selected from the group consisting of SEQ ID NO:21 and 23.

23. A chimeric gene comprising the nucleic acid fragment of Claim 21 operably linked to suitable regulatory sequences.

24. A transformed host cell comprising the chimeric gene of Claim 23.

25. A threonine synthase polypeptide comprising all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:22 and 24.

26. An isolated nucleic acid fragment encoding all or a substantial portion of a plant threonine synthase comprising a member selected from the group consisting of:

(a) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in SEQ ID NO:26;

(b) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in SEQ ID NO:26; and

(c) an isolated nucleic acid fragment that is complementary to (a) or (b).

27. The isolated nucleic acid fragment of Claim 26 wherein the nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in SEQ ID NO:25.

28. A chimeric gene comprising the nucleic acid fragment of Claim 26 operably linked to suitable regulatory sequences.

29. A transformed host cell comprising the chimeric gene of Claim 28.

30. A threonine synthase polypeptide comprising all or a substantial portion of the amino acid sequence set forth in SEQ ID NO:26.

31. An isolated nucleic acid fragment encoding all or a substantial portion of a plant threonine deaminase comprising a member selected from the group consisting of:

(a) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in SEQ ID NO:29;

(b) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in SEQ ID NO:29; and

(c) an isolated nucleic acid fragment that is complementary to (a) or (b).

32. The isolated nucleic acid fragment of Claim 31 wherein the nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in SEQ ID NO:28.

33. A chimeric gene comprising the nucleic acid fragment of Claim 31 operably linked to suitable regulatory sequences.

34. A transformed host cell comprising the chimeric gene of Claim 33.

35. A threonine deaminase polypeptide comprising all or a substantial portion of the amino acid sequence set forth in SEQ ID NO:29.

36. An isolated nucleic acid fragment encoding all or a substantial portion of a plant threonine deaminase comprising a member selected from the group consisting of:

(a) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:31 and 33;

(b) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:31 and 33; and

(c) an isolated nucleic acid fragment that is complementary to (a) or (b).

37. The isolated nucleic acid fragment of Claim 36 wherein the nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in a member selected from the group consisting of SEQ ID NO:30 and 32.

38. A chimeric gene comprising the nucleic acid fragment of Claim 36 operably linked to suitable regulatory sequences.

39. A transformed host cell comprising the chimeric gene of Claim 38.

40. A threonine deaminase polypeptide comprising all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:31 and 33.

41. An isolated nucleic acid fragment encoding all or a substantial portion of a plant S-adenosylmethionine synthetase wherein the nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in SEQ ID NO:35.

42. A chimeric gene comprising the nucleic acid fragment of Claim 41 operably linked to suitable regulatory sequences.

43. A transformed host cell comprising the chimeric gene of Claim 42.

44. An isolated nucleic acid fragment encoding all or a substantial portion of a plant S-adenosylmethionine synthetase wherein thc nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in SEQ ID NO:38.

45. A chimeric gene comprising the nucleic acid fragment of Claim 44 operably linked to suitable regulatory sequences.

46. A transformed host cell comprising the chimeric gene of Claim 45.

47. An isolated nucleic acid fragment encoding all or a substantial portion of a plant S-adenosylmethionine synthetase wherein the nucleotide sequence of the fragment comprises all or a portion of the sequence set forth in SEQ ID NO:41.

48. A chimeric gene comprising the nucleic acid fragment of Claim 47 operably linked to suitable regulatory sequences.

49. A transformed host cell comprising the chimeric gene of Claim 48.

50. A method of altering the level of expression of a plant amino acid biosynthetic enzyme in a host cell comprising:

(a) transforming a host cell with the chimeric gene of any of Claims 3, 8, 13, 18, 23, 28, 33, 38, 42, 45, and 48; and

(b) growing the transformed host cell produced in step (a) under conditions that are suitable for expression of the chimeric gene

wherein expression of the chimeric gene results in production of altered levels of a plant amino acid biosynthetic enzyme in the transformed host cell.

51. A method of obtaining a nucleic acid fragment encoding all or substantially all of the amino acid sequence encoding a plant amino acid biosynthetic enzyme comprising:

(a) probing a cDNA or genomic library with the nucleic acid fragment of any of Claims 1, 6, 11, 16, 21, 26, 31, 36, 41, 44, and 47;

(b) identifying a DNA clone that hybridizes with the nucleic acid fragment of any of Claims 1, 6, 11, 16, 21, 26, 31, 36, 41, 44, and 47;

(c) isolating the DNA clone identified in step (b); and

(d) sequencing the cDNA or genomic fragment that comprises the clone isolated in step (c)

wherein the sequenced nucleic acid fragment encodes all or substantially all of the amino acid sequence encoding a plant amino acid biosynthetic enzyme.

52. A method of obtaining a nucleic acid fragment encoding a portion of an amino acid sequence encoding a plant amino acid biosynthetic enzyme comprising:

(a) synthesizing an oligonucleotide primer corresponding to a portion of the sequence set forth in any of SEQ ID NOs:1, 3, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 28, 30, 32, 35, 38, and 41; and

(b) amplifying a cDNA insert present in a cloning vector using the oligonucleotide primer of step (a) and a primer representing sequences of the cloning vector

wherein the amplified nucleic acid fragment encodes a portion of an amino acid sequence encoding a plant amino acid biosynthetic enzyme.

53. The product of the method of Claim 51.

54. The product of the method of Claim 52.

55. A method for evaluating at least one compound for its ability to inhibit the activity of a plant biosynthetic enzyme selected from the group consisting of dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase and S-adenosylmethionine synthetase, the method comprising the steps of:

(a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding a plant biosynthetic enzyme selected from the group consisting of dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase and S-adenosylmethionine synthetase, operably linked to suitable regulatory sequences;

(b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of the biosynthetic enzyme encoded by the operably linked nucleic acid fragment in the transformed host cell;

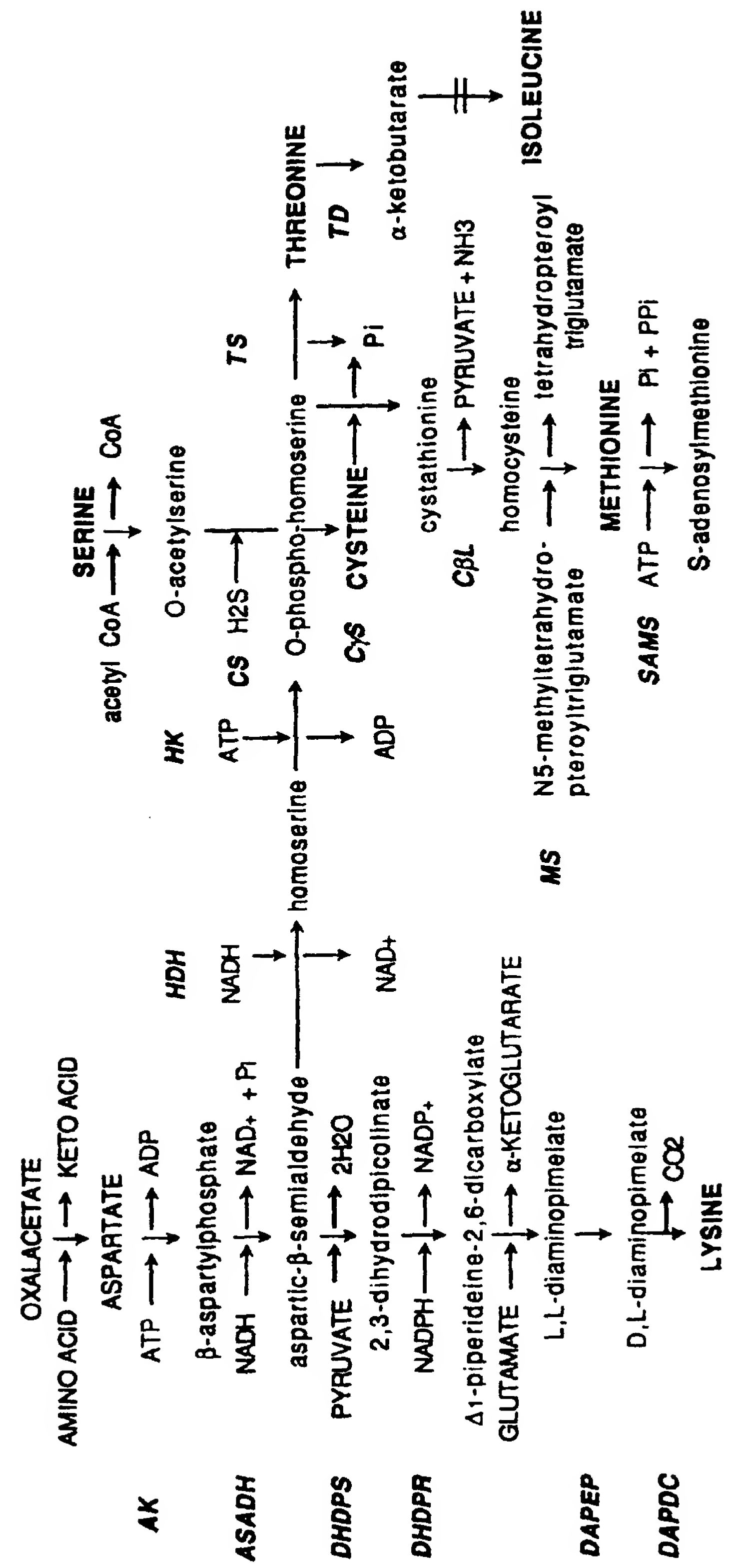
(c) optionally purifying the biosynthetic enzyme expressed by the transformed host cell;

(d) treating the biosynthetic enzyme with a compound to be tested; and

(e) comparing the activity of the biosynthetic enzyme that has been treated with a test compound to the activity of an untreated biosynthetic enzyme,

thereby selecting compounds with potential for inhibitory activity.

FIG.1



AK
ASADH
DHDPS
DHDPR
DAPEP
DAPDC
OXALACETATE
AMINO ACID
KETO ACID
ASPARTATE
ATP
ADP
β-aspartylphosphate
NADH
NAD+ + Pi
aspartic-β-semialdehyde
PYRUVATE
2H2O
2,3-dihydrodipicolinate
NADPH
NADP+
Δ1-piperideine-2,6-dicarboxylate
GLUTAMATE
α-KETOGLUTARATE
L,L-diaminopimelate
D,L-diaminopimelate
CO2
LYSINE
HDH
NADH
NAD+
homoserine
HK
ATP
ADP
O-phospho-homoserine
SERINE
acetyl CoA
CoA
O-acetylserine
CS
H2S
CYSTEINE
CγS
TS
THREONINE
Pi
TD
α-ketobutarate
ISOLEUCINE
cystathionine
CβL
PYRUVATE + NH3
homocysteine
MS
N5-methyltetrahydro-
pteroyltriglutamate
tetrahydropteroyl
triglutamate
METHIONINE
SAMS
ATP
Pi + PPi
S-adenosylmethionine

FIG.2

```
                 1                                                          60
SEQ ID NO:4      .................................................KIGRRNAA...
SEQ ID NO:2      ..............................................AGQISGMD.EPLEI
SEQ ID NO:5      MANQDLIPVVVNGAAGKMGREVIKAVAQAPDLQLVGAVDHNPSLQGQDIGEVVGIAPLEV

                 61                                                        120
SEQ ID NO:4      .......KVLCSTQMPPSQSTI.....KVVIIGATKEIGRTAIAAVSKARGMELAGAID.
SEQ ID NO:2      PVLNDLTMVLGSIAQSRATGVVVDFSEPSAVYDNVKQAAAFGLSSVVYVPKIELETVTEL
SEQ ID NO:5      PVLADLQSVLVLATQEKIQGVMVDFTHPSGVYDNVRSAIAYGVRPVVGTTGLSEQQIQDL

                 121                                                       180
SEQ ID NO:4      .......S.QCI...GLDAGEI..........................SGMGRTLEIPV.
SEQ ID NO:2      SAFCEKAS.GCLVAPTLSIGSVLLQQAAIQASFHYSNVEIVESRPNP.SDLPSQDAIQIA
SEQ ID NO:5      GDFAEKASTGCLIAPNFAIGVLLMQQAAVQACQYFDHVEIIELHHNQKADAPSGTAIKTA

                 181                                                       240
SEQ ID NO:4      ..LNDLTMV........LGSIAQTRA...............TGVV....VDFSEPSTVYD
SEQ ID NO:2      NNISDLGQIYNR...EDMDSSSPARGQLLGEDGVRVHSMVLPGLVSSTSINFSGPGEMYT
SEQ ID NO:5      QMLAEMGKTFNPPAVEEKETIAGAKGGL.GPGQIPIHSIRLPGLIAHQEVLFGSPGQLYT

                 241                                 276
SEQ ID NO:4      NVKQA...............................
SEQ ID NO:2      LRHDVANVQCLMPGLILAIRKVVRFKNLIYGLEKFL
SEQ ID NO:5      IRHDTTDRACYMPGVLLGIRKVVELKGLVYGLEKLL
```

FIG.3

```
             1                                                          60
SEQ ID NO: 7  L...........................................................
SEQ ID NO: 9  VS..........................................................
SEQ ID NO:11  MAITATISVPLTSPSRRTLTSVNSLSPLSTRSTLPTPQRTFKYPNSRLVVSSMSTETAVK
SEQ ID NO:13  ............................................................
SEQ ID NO:14  ............................................................

             61                                                        120
SEQ ID NO: 7  ............................................................
SEQ ID NO: 9  .......................................................GADGV
SEQ ID NO:11  TSSASFLNRKESGFLHFAKYHGLGNDFVLIDNRDSSEPKISAEKAVQLCDRNFGVGADGV
SEQ ID NO:13  .............ALHFVKYQGLGNDFIMVDNRDSAVPKVTPEEAAKLCDRNFGXGADGV
SEQ ID NO:14  ............MALSFSKYHGLGNDFILVDNRQSTEPCLTPDQAQQLCDRHFGIGADGV

             121                                                       180
SEQ ID NO: 7  .......................PEMCGNGVRCFARFIAEIENLQGTNRFTIHTGAGKIV
SEQ ID NO: 9  IFVMPGVNGADYTMRIFNSDGSEPEMCGNGVRCFARFIAELENLQGTHSFKIHTGAGLII
SEQ ID NO:11  IFVLPGISGTDYTMRIFNSDGSEPEMCGNGVRCFAKFVSQLENLHGRHSFTIHTGAGLII
SEQ ID NO:13  IFVLPGVNGADYTMRIFNSDGSNRNVWX.GFV............................
SEQ ID NO:14  IFALPGQGGTDYTMRIFNSDGSEPEMCGNGIRCLAKFLADLEGVEEK.TYRIHTLAGVIT

             181                                                       240
SEQ ID NO: 7  PEIQSDGQVKVDMGEPILSGLDIPTKLLATKNKAVVQAELAVEGLTWHVTCVSMGNPHCV
SEQ ID NO: 9  PEIQNDGKVKVDMGQPILAC........................................
SEQ ID NO:11  PEVLEDGNVRVDMGEPVLKALDVPTKLPANKDNAVVKSQLVVDGVIWHVTCVSMGNPHCV
SEQ ID NO:13  ............................................................
SEQ ID NO:14  PQLLADGQVKVDMGEPQLLAELIPTTLAPAGEK.VVDLPLAVAGQTWAVTCVSMGNPHCL
```

FIG.3 (Continued)

```
                 241                                                        300
SEQ ID NO: 7     TFGANELKVLQVDDLKLSEIGPKFEHHEMFPARTNTEFVQVLSRSHLKMRVWERGAGATL
SEQ ID NO: 9     ............................................................
SEQ ID NO:11     TFSREGSQNLLVDELKLAEIGPKFEHHEVFPARTNTEFVQVLSNSHLKMRVWERGAGATL
SEQ ID NO:13.................................................................
SEQ ID NO:14     TFVDD......VDSLNLTEIGPLFEHHPQFSQRTNTEFIQVLGSDRLKMRVWERGAGITL

                 301                                                       359
SEQ ID NO: 7     ACGTGACAVVVAAVLEGRAERKCVVDLPGGPLEIEWREDDNHVYMTGPAEVVFYGSVVH
SEQ ID NO: 9     ...........................................................
SEQ ID NO:11     ACGTGACATVVAAVLEGRAGRNCTVDLPGGPLQIEWREEDNHVYMTGSADVVYYGSLPL
SEQ ID NO:13     ............................................................
SEQ ID NO:14     ACGTGACATVVAAVLTGRGDRRCTVELPGGNLEIEWSAQDNRLYMTGPAQRVFSGQAEI
```

FIG.4

```
                1                                                          50
SEQ ID NO:24    ASSSLFQSLPFSLQTSK.PYAPPKPAAHFVVRA........QSPLTQNNNSSSKHRRPAD
SEQ ID NO:26    ............................................................
SEQ ID NO:27    LSSCLFNASVSSLNPKQDPIRRHRSTSLLRHRPVVISCTADGNNIKAPIETAVKPPHRTE

                61                                                        120
SEQ ID NO:20    .........................................MENGAATNGASEKSHSPS
SEQ ID NO:22    ............................................................
SEQ ID NO:24    ENIRDEARRINAPHDHHLFSAKYVPFNADSSSSSSTESYSLDEIVYRSQSGGLLDVQHDM
SEQ ID NO:26    ............................................................
SEQ ID NO:27    DNIRDEARR.NRSNAVNPFSAKYVPFNA...APGSTESYSLDEIVYRSRSGGLLDVEHDM

                121                                                       180
SEQ ID NO:16    ............................................................
SEQ ID NO:18    ............................................................
SEQ ID NO:20    QTYLSTRGDDYGLSFETVV.........................................
SEQ ID NO:22    ............................................................
SEQ ID NO:24    DALKRFDGEYWRNLFDSRVGKTTWPYGSGVWSKKEWVLPEIHDDDIVSAFEGNSNLFWAE
SEQ ID NO:26    ............................................................
SEQ ID NO:27    EALKRFDGAYWRDLFDSRVGKSTWPYGSGVWSKKEWVLPEIDDDDIVSAFEGNSNLFWAE

                181                                                       240
SEQ ID NO:16    ..................................................VGCASTGDTSA
SEQ ID NO:18    ............................................................
SEQ ID NO:20    LKGLAADGGLFLPEEVPAATEWQSWKDLPYTELAVKV.......................
SEQ ID NO:22    ............................................................
SEQ ID NO:24    RFGKQFLGMNDLWVKHCGISHTGSFKDLGMTVLVSQVNRLRKMNRPVVGVGCASTGDTSA
SEQ ID NO:26    ............................................................
SEO ID NO:27    RFGKQFLGMNDLWVKHGGISHTGSFKDLGMTVLVSQVNRLRKMKRPVVGVGCASTGDTSA
```

FIG.4 (Continued)

```
               241                                                        300
SEQ ID NO:16   ALSAYCAAAGIPAIVFLPADRISLQQLIQPIANGATVLSLDTDFDGCMRLIREVTAELPI
SEQ ID NO:18   ............................................................
SEQ ID NO:20   .LSLYISPAEVPTE........DLRALVER..............................
SEQ ID NO:22   ............................................................
SEQ ID NO:24   ALSAYCASAAIPSIVFLPANKISLAQLVQPIANGAFVLSIDTDFDGCMQLIREVTAELPI
SEQ ID NO:26   ..........................LIQPIANGATVLSLDTDFDGCMRLIREVTAELPI
SEQ ID NO:27   ALSAYCASAGIPSIVFLPANKISMAQLVQPIANGAFVLSIDTDFDGCMKLIREITAELPI

               301                                                        360
SEQ ID NO:16   YLANSLNPL.RLEGQKTAAIEILQQFNWQVPDWVIVPGGNLGNIYAFYKGFEMCRVLGLV
SEQ ID NO:18   ............................................................
SEQ ID NO:20   ..............SYSTFRSKEVVPLVKLEDNLHLLELFHGPNYSF.............
SEQ ID NO:22   ............................................................
SEQ ID NO:24   YLANSLNSL.KLEGQKTAAIEILQQFDWQVPDWVIVPGSNLGNIYAFYKGFKMFQELGLV
SEQ ID NO:26   YLANSLNSL.XLEGQKTAAIRDIATXNWQVPGLGHIPRRQSXTFYAFLQGF.........
SEQ ID NO:27   YLANSLNSL.RLEGQKTAAIEILQQFDWQVPDWVIVPGGNLGNIYAFYKGFKMCQELGLV

               361                                                        420
SEQ ID NO:16   DRVPRLVCAQAANANPLYRYYKSGWTEFEPQTAETTFASAIQIGDPVSVDRAVVALKATD
SEQ ID NO:18   ............................................................
SEQ ID NO:20   .............................KDCALQFLGNLXEYF................
SEQ ID NO:22   ............................................................
SEQ ID NO:24   DKIPRLVCAQAANADPLYLYFKSGWKEFKPVKSSTTFASAIQIGDPVSIDRAVHALKSCD
SEQ ID NO:26   ............................................................
SEQ ID NO:27   DRIPRMVCAQAANANPLYLHYKSGWKDFKPMTASTTFASAIQIGDPVSIDRAVYALKKCN

               421                                                        480
SEQ ID NO:16   GIVEEATEEELMDATALADRTGMFACPHTGVALAALFKLQGQRIIGPNDRTVVVSTAHGL
SEQ ID NO:18   ............................................................
SEQ ID NO:20   ............................................................
SEQ ID NO:22   ............DAMVQADSTGMFICPHTGVALAALIKLRNRGVIGAGERVVVVSTAHGL
SEQ ID NO:24   GIVEEATEEELMDATAQADSTGMFICPHTGVALTALFKLRNSGVIKATDRTVVVSTAHGL
SEQ ID NO:26   ............................................................
```

FIG.4 (Continued)

```
SEQ ID NO:27   GIVEEATEEELMDAMAQADSTGMFICPHTGVALTALFKLRNQGVIAPTDRTVVVSTAHGL

               481                                                     537
SEQ ID NO:16   KFTQSKIDYHDKNIKDMVCQYANPPISVKADFGSVMDVLQKN.......LNGKI...
SEQ ID NO:18   ................MACKYSNPPVSVKADFGAVMDVLKKR.......LKGKL...
SEQ ID NO:20   .........................................................
SEQ ID NO:22   KFAQSKIDYHSGLIPGMG.RYANPLVSVKADFGSVMDVLKDSCTTSPPTLTSLDVAK
SEQ ID NO:24   KFTQSKIDYHSKDIKDMACRYANPPMQVKADFGSVMDVLKTY.......LQSKA..H
SEQ ID NO:26   .........................................................
SEQ ID NO:27   KFTQSKIDYHSNAIPDMACRFSNPPVDVKADFGAVMDVLKSY.......LGSNTLTS
```

FIG.5

```
                1                                                           60
SEQ ID NO:29    ............................................................
SEQ ID NO:31    ............................................................
SEQ ID NO:33    ............................................................
SEQ ID NO:34    MASHDYLKKILTARVYDVAFETELEPARNLSARLRNPVYLKREDNQPVFSFKLRGAYNKM

                61                                                         120
SEQ ID NO:29    .....................................................TVVLEGD
SEQ ID NO:31    ............................................................
SEQ ID NO:33    ............................................................
SEQ ID NO:34    AHIPADALARGVITASAGNHAQGVAFSAARMGVKAVIVVPVTTPQVKVDAVRAHGGPGVE

                121                                                        180
SEQ ID NO:29    SYDEAQSYAK.....LRCQQE.GRTFVPPFDHPDVITGQGTIGMEIVRQLQGPLHAIFVP
SEQ ID NO:31    ............................................................
SEQ ID NO:33    ............................................................
SEQ ID NO:34    VIQAGESYSDAYAHALKVQEERGLTFVHPFDDPYVIAGQGTIAMEILRQHQGPIHAIFVP

                181                                                        240
SEQ ID NO:29    VGGGGLIAGIAAYVKRVRPEVKIIGVEPSDANAMALSLCHGKRVMLEHVGGFADGVAVKA
SEQ ID NO:31    ............................................................
SEQ ID NO:33    ............................................................
SEQ ID NO:34    IGGGGLAAGVAAYVKAVRPEIKVIGVQAEDSCAMAQSLQAGKRVELAEVGLFADGTAVKL

                241                                                        300
SEQ ID NO:29    VGEETFRLCRELVDGIVMVSRDAICASIKDMFEEKRSILEPAGALALAGAEAYCKYYNLK
SEQ ID NO:31    ............................................................
SEQ ID NO:33    ............................................................
SEQ ID NO:34    VGEETFRLCKEYLDGVVTVDTDALCAAIKDVFQDTRSVLEPSGALAVAGAKLYAEREGIE
```

FIG.5 (Continued)

```
                301                                                        360
SEQ ID NO:29    GETVVAITSGANMNFDRLRLVTELADVGRKREAVLATFLPERQGSFKKFTELVGRMNITE
SEQ ID NO:31    ..NIVAITSGANMNFDKLRVVTELANVGRKQEAVLATVMAEEPGSFKQFCELVGQMNITE
SEQ ID NO:33    ............................................................
SEQ ID NO:34    NQTLVAVTSGANMNFDRMRFVAERAEVGEAREAVFAVTIPEERGSFKRFCSLVGDRNVTE

                361                                                        420
SEQ ID NO:29    FKYRYDSNAKDALVLYSVGIYTDNELGAMMDRMESAKLRTVNLTDNDLAKDHLRYFIGGR
SEQ ID NO:31    FKYRYNSNEK.AVVLYSVGVHTISELRAMQERMESSQLKTYNLTESDLVKDHLRYLMGGR
SEQ ID NO:33    ............................................................
SEQ ID NO:34    FNYRI.ADAQSAHIFVGVQIRRRGESADIAANFESHGFKTADLTHDELSKEHIRYMVGGR

                421                                                        480
SEQ ID NO:29    SEIK.DELVYRFIFPERPGALMKFLDTFSPRWNISLFHYRAQGEAGANVLVGIQVPPAEF
SEQ ID NO:31    SNVQ.NEVFVVSPXPRKTGALMKFLDXFSPRWDISL........................
SEQ ID NO:33    ................RPGALMKFLDPFSPRWNISLFHYRGEGETGANVLVGIQVPKSEM
SEQ ID NO:34    SPLALDERLFRFEFPERPGALMKFLSSMAPDWNISLFHYRNQGADYSSILVGLQVPQADH

                481                            512
SEQ ID NO:29    DEFKSHANNLGYEYMSEHNNEIYRLLLRDPKV
SEQ ID NO:31    ................................
SEQ ID NO:33    DEFHDRANKLGYDYKVVNNDDDFQLLMH....
SEQ ID NO:34    AEFERFLAALGYPYVEESANPAYRLFLS....
```

FIG.6

```
SEQ ID NO:36   126 GCAGATCAAAGAAGATGGCAGCTCTCGACACCTTCCTCTTCACCTCGGAGTCTGTGAACG 185
                   ||||||   |||||||||| || || || ||||||||||| |||||||||||||||||||
SEQ ID NO:37   774 GCAGATAGGAGAAGATGGCCGCACTTGATACCTTCCTCTTTACCTCGGAGTCTGTGAACG 833

SEQ ID NO:36   186 AGGGACACCCTGACAAGCTCTGCGACCAGGTCTCAGATGCCGTTCTTGACGCTTGCCTTG 245
                   |||| ||||||||||||||||||||||| ||||||||||| || ||||| || ||||| |
SEQ ID NO:37   834 AGGGCCACCCTGACAAGCTCTGCGACCAAGTCTCAGATGCTGTGCTTGATGCCTGCCTCG 893

SEQ ID NO:36   246 CTGAGGACCCTGACAGCAAGGTTGCTTGTGAGACCTGCACCAAGACCAACATGGTCATGG 305
                   | |||||||||||||||||||| ||||||||||||||||||||||| |||||||||||||
SEQ ID NO:37   894 CCGAGGACCCTGACAGCAAGGTCGCTTGTGAGACCTGCACCAAGACAAACATGGTCATGG 953

SEQ ID NO:36   306 TCTTTGGTGAGATCACCACCAAGGCCAATGTCGACTACGAGAAGATTGTCAGGGAGACCT 365
                   ||||||||||||||||||||||||| || || ||||| |||||||||||||||||||| |
SEQ ID NO:37   954 TCTTTGGTGAGATCACCACCAAGGCTAACGTTGACTATGAGAAGATTGTCAGGGAGACAT 1013

SEQ ID NO:36   366 GCCGCAACATTGGTTTTGTGTCAAACGATGTCGGGCTTGACGCTGACCACTGCAAGGTGC 425
                   |||| ||||| ||||||||||||   |||||||| || || |||||||||||||||||||
SEQ ID NO:37  1014 GCCGTAACATCGGTTTTGTGTCAGCTGATGTCGGTCTCGATGCTGACCACTGCAAGGTGC 1073

SEQ ID NO:36   426 TCGTGAACATTGAGCAGCAGTCCCCTGATATTGCTCAGGGTGTGCATGGCCACTTCACCA 485
                   | |||||||| ||||||||||||||||| ||||| ||||||||||| || ||||||||||
SEQ ID NO:37  1074 TTGTGAACATCGAGCAGCAGTCCCCTGACATTGCACAGGGTGTGCACGGGCACTTCACCA 1133

SEQ ID NO:36   486 AGCGCCCCGAGGAGATTGGAGCTGGTGACCAGGGACACATGTTCGGGTATGCGACCGATG 545
                   ||||||| ||||||||||| ||||||||||||||||||||||| || ||||| || ||||
SEQ ID NO:37  1134 AGCGCCCTGAGGAGATTGGTGCTGGTGACCAGGGACACATGTTTGGATATGCAACTGATG 1193

SEQ ID NO:36   546 AGACCCCTGAGTTGATGCCCCTCAGCCATGTCCTTGCCACCAAGCTAGGTGCTCGTCTCA 605
                   ||||||||||||||||||||||||||||||||||||| |||||||| || |||||||| |
SEQ ID NO:37  1194 AGACCCCTGAGTTGATGCCCCTCAGCCATGTCCTTGCTACCAAGCTTGGCGCTCGTCTTA 1253
```

FIG.6 (Continued)

```
SEQ ID NO:36   606 CCGAGGTCCGCAAGAACGGAACCTGCCCCTGGCTCAGGCCTGATGGGAAGACCCAGGTGA 665
SEQ ID NO:37  1254 CGGAGGTTCGCAAGAATGGACCTGCGCATGGCTCAGGCCTGACGGGAAGACCCAAGTGA 1313

SEQ ID NO:36   666 CAGTCGAGTACCGCAATGAGGGTGGTGCCATGGTCCCCATCCGTGTCCACACCGTCCTCA 725
SEQ ID NO:37  1314 CTGTTGAGTACCGCAATGAGAGCGGTGCCAGGGTCCCTGTCCGTGTCCACACCGTCCTCA 1373

SEQ ID NO:36   726 TCTCCACCCAGCACGACGAGACAGTGACCAATGATGAGATCGCTGCTGACCTGAAGGAGC 785
SEQ ID NO:37  1374 TCTCTACCCAGCATGATGAGACAGTCACCAACGATGAGATTGCTGCTGACCTGAAGGAGC 1433

SEQ ID NO:36   786 ATGTCATCAAGCCTATCATCCCTGAGCAGTACCTTGACGAGAAGACCATCTTCCACCTTA 845
SEQ ID NO:37  1434 ATGTCATCAAGCCTGTCATTCCCGAGCAGTACCTTGATGAGAAGACAATCTTCCATCTTA 1493

SEQ ID NO:36   846 ACCCATCCGGCCGCTTTGTCATTGGTGGACCTCACGGCGATGCTGGCCTCACTGGCCGCA 905
SEQ ID NO:37  1494 ACCCATCTGGTCGCTTCGTCATTGGCGGACCTCATGGTGATGCTGGTCTCACTGGCCGGA 1553

SEQ ID NO:36   906 AGATCATCATTGACACCTACGGTGGCTGGGGAGCCCATGGCGGTGGCGCTTTCTCCGGCA 965
SEQ ID NO:37  1554 AGATCATCATTGACACTTATGGTGGCTGGGGAGCTCACGGTGGTGGTGCCTTCTCTGGCA 1613

SEQ ID NO:36   966 AGGACCCAACCAAGGTTGACCGCAGCGGAGCCTATGTCGCGAGGCAGGCTGCCAAGAGCA 1025
SEQ ID NO:37  1614 AGGACCCAACCAAGGTTGACCGCAGTGGAGCATACGTCGCAAGGCAAGCTGCCAAGAGCA 1673

SEQ ID NO:36  1026 TCGTCGCCAGCGGCCTTGCTCGCCGCGCCATCGTCCAGGTGTCCTACGCCATCGGCGTGC 1085
SEQ ID NO:37  1674 TTGTTGCTAGTGGCCTTGCTCGCCGCTGCATTGTCCAAGTATCATACGCCATCGGTGTCC 1733
```

FIG.6 (Continued)

```
SEQ ID NO:36 1086 CCGAGCCTCTCTCCGTGTTTGTCGACACGTACGGCACCGGCGCGATCCCCGACAAGGAGA 1145
                  | ||||| || ||||| || |||||||| |||||||| |||  |||||| ||||||||||
SEQ ID NO:37 1734 CAGAGCCACTGTCCGTATTCGTCGACACATACGGCACTGGCAGGATCCCTGACAAGGAGA 1793

SEQ ID NO:36 1146 TCCTCAAGATTGTCAAGGAGAACTTCGATTTCAGGCCTGGCATGATTATCATCAACCTTG 1205
                  ||||||||||||| |||||||||||||| ||||||||||||||||| |||||||||||||
SEQ ID NO:37 1794 TCCTCAAGATTGTGAAGGAGAACTTCGACTTCAGGCCTGGCATGATCATCATCAACCTTG 1853

SEQ ID NO:36 1206 ACCTCAAGAAAGGCGGCAACGGGCGCTACCTCAAGACGGCAGCCTACGGCCACTTCGGAA 1265
                  |||||||||||||||||||||| ||||||||||||||||| || ||||| ||||||||||
SEQ ID NO:37 1854 ACCTCAAGAAAGGCGGCAACGGACGCTACCTCAAGACGGCGGCTTACGGTCACTTCGGAA 1913

SEQ ID NO:36 1266 GGGACGACCCTGACTTCACCTGGGAGGTGGTGAAGCCACTCAAGTCGGAGAAACCTTCTG 1325
                  |||||||||| |||||||||||||||||||||||||| ||||||| |||||| |||||||
SEQ ID NO:37 1914 GGGACGACCCAGACTTCACCTGGGAGGTGGTGAAGCCCCTCAAGTGGGAGAAGCCTTCTG 1973

SEQ ID NO:36 1326 CCTAAGGCGGCCTTTT 1341
                  |||||     || |||
SEQ ID NO:37 1974 CCTAAAAGCTCCCTTT 1989
```

FIG.7

```
SEQ ID NO:38    80 GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGGACACCCTGACAAGCTCTGCGAC 139
SEQ ID NO:40   123 GAAACTTTCTTATTCACCTCCGAGTCTGTGAACGAGGGTCACCCAGACAAGCTCTGTGAT 182

SEQ ID NO:38   140 CAAATCTCCGATGCTGTCCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199
SEQ ID NO:40   183 CAGATCTCTGATGCAGTTCTTGATGCCTGCCTTGAGCAAGATCCCGAGAGCAAAGTTGCA 242

SEQ ID NO:38   200 TGCGAAACATGCACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACCACCAAGGCC 259
SEQ ID NO:40   243 TGTGAAACTTGCACCAAGACCAACTTGGTCATGGTCTTTGGTGAGATCACAACCAAGGCT 302

SEQ ID NO:38   260 AACGTTGACTACGAGAAGATCGTGCGTGACACCTGCAGGAACATCGGCTTCGTCTCAAAC 319
SEQ ID NO:40   303 ATTGTAGACTATGAGAAGATTGTGCGTGACACATGCCGTAATATTGGATTTGTTTCTGAT 362

SEQ ID NO:38   320 GATGTGGGACTTGATGCTGACAACTGCAAGGTCCTTGTAAACATTGAGCAGCAGAGCCCT 379
SEQ ID NO:40   363 GATGTTGGTCTTGATGCTGACAACTGCAAGGTCCTTGTTTACATTGAGCAGCAAAGTCCT 422

SEQ ID NO:38   380 GATATTGCCCAGGGTGTGCACGGCCACCTTACCAAAAGACCCGAGGAAATCGGTGCTGGA 439
SEQ ID NO:40   423 GATATTGCTCAAGGTGTCCACGGCCATCTGACCAAACGCCCCGAGGAGATTGGTGCTGGT 482

SEQ ID NO:38   440 GACCAGGGTCACATGTTTGGCTATGCCACGGACGAAACCCCAGAATTGATGCCATTGAGT 499
SEQ ID NO:40   483 GACCAGGGCCACATGTTTGGCTATGCAACAGATGAGACCCCTGAATTAATGCCTCTCAGT 542

SEQ ID NO:38   500 CATGTTCTTGCAACTAAACTCGGTGCTCGTCTCACCGAGGTTCGCAAGAACGGAACCTGC 559
SEQ ID NO:40   543 CACGTGCTTGCAACTAAACTTGGTGCCCGTCTTACAGAAGTCCGCAAGAATGGCACCTGC 602
```

FIG.7 (Continued)

```
SEQ ID NO:38   560 CCATGGTTGAGGCCTGATGGGAAAACCCAAGTGACTGTTGAGTATTACAATGACAACGGT 619
SEQ ID NO:40   603 GCCTGGTTGAGGCCTGATGGCAAGACCCAAGTTACTGTTGAGTATAGCAATGACAATGGT 662

SEQ ID NO:38   620 GCCATGGTTCCAGTTCGTGTCCACACTGTGCTTATCTCCACCCAACATGATGAGACTGTG 679
SEQ ID NO:40   663 GCCATGGTTCCAATTAGGGTACACACTGTTCTTATCTCCACCCAACACGATGAGACCGTT 722

SEQ ID NO:38   680 ACCAACGACGAAATTGCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGATCCCGGAG 739
SEQ ID NO:40   723 ACCAATGATGAGATTGCCCGCGACCTTAAGGAGCATGTCATCAAACCAGTCATCCCAGAG 782

SEQ ID NO:38   740 AAGTACCTTGATGAGAAGACCATTTTCCACTTGAACCCCTCTGGCCGTTTTGTCATTGGA 799
SEQ ID NO:40   783 AAGTACCTTGATGAGAATACTATTTTCCACCTTAACCCATCTGGCCGATTCGTTATTGGT 842

SEQ ID NO:38   800 GGTCCTCACGGTGATGCTGGTCTCACCGGCCGCAAGATCATCATCGATACTTACGGAGGA 859
SEQ ID NO:40   843 GGACCTCATGGTGATGCTGGTCTCACTGGTCGTAAAATCATCATCGACACTTATGGTGGT 902

SEQ ID NO:38   860 TGGGGTGCTCATGGTGGTGGTGCTTTCTCCGGGAAGGATCCCACCAAGGTTGATAGGAGT 919
SEQ ID NO:40   903 TGGGGTGCTCATGGTGGTGGTGCTTTCTCGGGCAAAGACCCAACCAAGGTCGACAGGAGT 962

SEQ ID NO:38   920 GGTGCTTACATTGTGAGACAGGCTGCTAAGAGCATTGTGGCAAGTGGACTAGCCAGAAGG 979
SEQ ID NO:40   963 GGTGCATACATTGTAAGGCAGGCTGCAAAGAGTATCGTAGCTAGTGGACTTGCTCGTAGA 1022

SEQ ID NO:38   980 TGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCCCGAGCCTTTGTCTGTCTTTGTTGAC 1039
SEQ ID NO:40  1023 TGCATCGTGCAGGTATCTTATGCCATCGGTGTGCCTGAGCCATTGTCTGTATTCGTTGAC 1082
```

FIG.7 (Continued)

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SEQ ID NO:38 1040 ACCTATGGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGAACTTT 1099
                  ||||||||||| || ||||||| ||| | ||| ||| | || || || ||||||||||||
SEQ ID NO:40 1083 ACCTATGGCACTGGAAAGATCCCTGACAGGGAAATTTTGAAGATCGTTAAGGAGAACTTT 1142

SEQ ID NO:38 1100 GATTTCAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGG 1159
                  || ||||| || || ||||| ||||| ||| | ||| | ||||||||||| ||||  ||
SEQ ID NO:40 1143 GACTTCAGACCTGGAATGATGTCCATTAACTTGGATTTGAAGAGGGGTGGCAATAGAAGA 1202

SEQ ID NO:38 1160 TTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACCCTGACTTCACATGGGAA 1219
                  |||||||| |||||||| ||||| ||||| ||  | || ||||| || ||||||||||||
SEQ ID NO:40 1203 TTCTTGAAAACTGCTGCCTATGGTCACTTTGGACGTGATGACCCCGATTTCACATGGGAA 1262

SEQ ID NO:38 1220 GTGGTCAAGCCCCTCAAGTGGGAGAAGGCCTAAGGCCATTCATTCCACTGCAATGTGCTG 1279
                  || |||||||||||||||||||| ||| || ||| | | | | | |    | ||||  |
SEQ ID NO:40 1263 GTTGTCAAGCCCCTCAAGTGGGAAAAGCCCCAAGACTAATAAGTGCTTGCCTATGTTTTT 1322

SEQ ID NO:38 1280 GGAGTTTTTT 1289
                  |   ||| ||
SEQ ID NO:40 1323 GTTCTTTGTT 1332
```

FIG.8

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SEQ ID NO:42    41 AGCAGCGCAAGGGCATCGCTAGCACTAAAGAAATGGCAGCCGAGACGTTCCTCTTCACGT 100
SEQ ID NO:43    23 AACTGCACGAGAGCATCTCTACCACCAAAGAAATGGCGGCCGAGACGTTCCTCTTCACGT 82

SEQ ID NO:42   101 CCGAGTCTGTGAACGAGGGCCATCCCGACAAGCTCTGTGACCAAGTCTCCGACGCCGTCT 160
SEQ ID NO:43    83 CCGAGTCCGTGAACGAGGGCCATCCCGACAAGCTGTGCGACCAGGTCTCTGACGCCGTCT 142

SEQ ID NO:42   161 TGGATGCCTGCTTGGCCCAGGATGCCGACAGCAAGGTCGCCTGCGAGACCGTCACCAAGA 220
SEQ ID NO:43   143 TGGACGCCTGCTTGGCCCAGGATCCTGACAGCAAGGTTGCTTGCGAGACCTGCACCAAGA 202

SEQ ID NO:42   221 CCAACATGGTCATGGTCTTGGGCGAGATCACCACCAAGGCCACCGTCGACTATGAGAAGA 280
SEQ ID NO:43   203 CCAACATGGTCATGGTCTTCGGCGAGATCACCACCAAGGCCACCGTTGACTATGAGAAGA 262

SEQ ID NO:42   281 TCGTGCGTGACACCTGCCGCAACATCGGTTTCATCTCTGATGACGTTGGTCTCGACGCCG 340
SEQ ID NO:43   263 TTGTGCGCGACACCTGCCGTGACATCGGCTTCATCTCTGACGACGTCGGTCTCGATGCCG 322

SEQ ID NO:42   341 ACCGTTGCAARGTGCTCGTCAACATCGAGCAGCAGTCCCCTGACATTGCCCAGGGTGTTC 400
SEQ ID NO:43   323 ACCATTGCAAGGTGCTCGTCAACATCGAGCAGCAATCCCCTGACATTGCCCAGGGTGTTC 382

SEQ ID NO:42   401 ATGGACACTTCACCAAGCGTCCCGAAGAAGTCGGCGCCGGTGACCAGGGCATCATGTTCG 460
SEQ ID NO:43   383 ACGGACACTTCACCAAGCGTCCAGAAGAGGTCGGCGCCGGTGACCAGGGCATCATGTTTG 442
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FIG.8 (Continued)

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SEQ ID NO:42   461 GCTATGCCACCGATGAGACCCCTGAGCTGATGCCCCTCAAGCACGTGCTTGCCACCAAGC 520
SEQ ID NO:43   443 GCTACGCCACTGATGAGACCCCTGAGCTGATGCCCCTCACCCACATGCTTGCCACCAAGC 502

SEQ ID NO:42   521 TYGGAGCTCGCCTCACSGAGGTCCGCAAGAATGGCACCTGCGCCTGGGTCAGGCCTGACG 580
SEQ ID NO:42   503 TCGGAGCTCGCCTCACCGAGGTCCGCAAGAATGGCACCTGCGCCTGGCTCAGGCCTGATG 562

SEQ ID NO:42   581 GAAAGACCCAGGTCACAGTCGAGTACCTAAACGAGGATGGTGCCATGGTACCTGTTCGTG 640
SEQ ID NO:43   563 GAAAGACCCAGGTCACCATTGAGTACCTAAACGAGGGTGGTGCCATGGTGCCCGTTCGTG 622

SEQ ID NO:42   641 TGCACACCGTCCTCATCTCCACCCAGCACGACGAGACCGTCACCAACGACGAGATTGCTG 700
SEQ ID NO:43   623 TGCACACCGTCCTCATCTCCACCCAGCATGATGAGACCGTCACCAACGATGAGATCGCTG 682

SEQ ID NO:42   701 CGGACCTCAAGGAGCATGTCATCAAGCCGGTGATCCCCGCAAAGTACCTCGATGAGAACA 760
SEQ ID NO:43   683 CAGACCTCAAGGAGCATGTCATCAAGCCGGTGATTCCCGGGAAGTACCTCGATGAGAACA 742

SEQ ID NO:42   761 CCATCTTCCACCTGAACCCGTCTGGCCGCTTCGTCATCGGCGGCCCCCACGGTGACGCCG 820
SEQ ID NO:43   743 CCATCTTCCACCTGAACCCATCGGGCCGCTTTGTCATCGGTGGCCCTCACGGCGATGCCG 802

SEQ ID NO:42   821 GTCTCACCGGCCGCAAGATCATCATCGACACCTATGGTGGCTGGGGAGCCCACGGCGGCG 880
SEQ ID NO:43   803 GTCTCACCGCCCGCAAGATCATCATCGACACCTATGGTGGCTGGGGAGCCCACGGCGGCG 862

SEQ ID NO:42   881 GTGCCTTCTCTGGCAAGGACCCAACCAAGGTCGACCGYAGTGGCGCCTACATTGCCAGGC 940
SEQ ID NO:43   863 GTGCCTTCTCTGGCAAGGACCCTACCAAGGTCGACCGCAGTGGCGCCTACATTGCCAGGC 922
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FIG.8 (Continued)

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SEQ ID NO:42  941 ARGCCGCCAAGAGCATCATCGCCAGCGGCCTCGCACGCCGCTGCATTGTGCAGATCTCAT 1000
                  | || ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
SEQ ID NO:43  923 AGGCTGCCAAGAGCATCATCGCCAGCGGCCTCGCACGCCGGTGCATTGTGCAGATCTCAT 982

SEQ ID NO:42 1001 ACGCCATCGGTGTGCCTGAGCCTTTGTCTGTGTTCGTCGACTCCTACGGCACCGGCAAGA 1060
                  | ||||||||||| |||||||||||||||||||||||||||||||||||||| |||||||
SEQ ID NO:43  983 ATGCCATCGGTGTACCTGAGCCTTTGTCTGTGTTCGTCGACTCCTACGGCACTGGCAAGA 1042

SEQ ID NO:42 1061 TCCCCGACAGGGAGATCCTCAAGCTCGTGAAGGAGAACTTTGACTTCAGGCCCGGGATGA 1120
                  |||| |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
SEQ ID NO:43 1043 TCCCTGACAGGGAGATCCTCAAGCTCGTGAAGGAGAACTTTGACTTCAGACCCGGGATGA 1102

SEQ ID NO:42 1121 TCAGCATCAACCTGGACTTGAAGAAAGGTGGAAACAGGTTCATCAAGACCGCTGCTTACG 1180
                  |||  |||||||| ||||||||||||||||||||||||||||||||||| ||||||||||
SEQ ID NO:43 1103 TCACGATCAACCTCGACTTGAAGAAAGGTGGAAACAGGTTCATCAAGACAGCTGCTTACG 1162

SEQ ID NO:42 1181 GTCACTTTGGCCGTGATGATGCCGACTTCACCTGGGAGGTGGTGAAGCCCCTCAAGTTCG 1240
                  ||||||||||||| |||||||| |||||||||||||||||||||||||||||||||||||
SEQ ID NO:43 1163 GTCACTTTGGCCGCGATGATGCTGACTTCACCTGGGAGGTGGTGAAGCCCCTCAAGTTCG 1222

SEQ ID NO:42 1241 ACAAGGCATCTGCCTAAGAGCATGGCAT 1268
                  ||||||||||||| |||||  | | |||

SEQ ID NO:43 1223 ACAAGGCATCTGCTTAAGAAGAAGACAT 1250

SEQ ID NO:42 1271 TCTTGGTCTGCCGCCTCTCAAGTTCGTCAAGACGGGATCATGTTGCTCCTGGGAAGTGGG 1330
                  ||||||||||  |||||||||||||| |||| ||||||| | |||||||| ||||||  |
SEQ ID NO:43 1266 TCTTGGTCTGATGCCTCTCAAGTTCGGCAAGGCGGGATCCTTTTGCTCCTCGGAAGTAAG 1325

SEQ ID NO:42 1331 AAGAAGCATTAGACATTG 1348
                  ||||||||||  |||| |
SEQ ID NO:43 1326 AAGAAGCATTCAACATCG 1343
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